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version 6.2.1 - 2007 Biocceleration Ltd.
GenCore (c) 1993
            Copyright
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protein search, using sw model OM protein

April 25, 2007, 03:54:56 ; Search time 108 Seconds (without alignments) 564.248 Million cell updates/sec Run on:

US-10-665-383-2

score:

Sequence:

1 QVQLVQSGAEVKKPGASVKV.....vpyYYGMDVWGQGTTVTVSS 125 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2782304 seqs, 489333398 residues Searched:

2782304 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003bs:\* geneseqp2007s:\* geneseqp2003as:\* geneseqp20068:\* A\_Geneseq\_200701:\* 1: genesecn10000: geneseqp2004s:\* geneseqp1990s:\* geneseqp2002s:\* geneseqp2005s:\* geneseqp2000s:\* geneseqp2001s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Adk18776 Anti-huma	Adk18948 Anti-huma	Adk18624 Anti-huma	Adk18813 Anti-huma	Adl25392 Human mAb	Adk18614 Anti-huma	Adk18779 Anti-huma	Adk18919 Anti-huma	Adk18816 Anti-huma	Adl25444 Human mAb	Adk18864 Anti-huma	Adk18595 Anti-huma	Adk18777 Anti-huma	Adl25408 Human mAb	Aek98538 Human ant	Adk18814 Anti-huma	Aeh94456 Anti-ten-	Adk18925 Anti-huma	Adk18780 Anti-huma	Adk18616 Anti-huma	Adk18817 Anti-huma	Adl25448 Human mAb
	a	ADK18776	ADK18948	ADK18624	ADK18813	ADL25392	ADK18614	ADK18779	ADK18919	ADK18816	ADL25444	ADK18864	ADK18595	ADK18777	ADL25408	AEK98538	ADK18814	AEH94456	ADK18925	ADK18780	ADK18616	ADK18817	ADL25448
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de	Query Match	100.0	100.0	100.0	100.0	100.0	94.9	94.9	94.9	94.9	94.9	88.3	88.3	88.3	88.3	87.5	86.2	86.0	85.6	85.6	85.6	85.6	85.6
	Score	672	672	672	672	672	638	638	638	638	638	593.5	593.5	593.5	593.5	588	579.5	. 578	575.5	575.5	575.5	575.5	575.5
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Adk18620 Anti-huma Adk18818 Anti-huma Adk18781 Anti-huma	Adk18936 Antı-numa Adl25456 Human mAb Aek98534 Human ant	Aei64964 Anti-Ang- Aei64968 Anti-Ang- Adk18597 Anti-Anma	Adk18870 Anti-huma Adk18812 Anti-huma	Adk18775 Anti-huma Ad125412 Human mAb	Aej20382 Anti-IRTA Aem14838 Human ant	Aem14842 Human ant Abr55829 Heavy cha	Aeg17553 Human ang Adk18778 Anti-huma	Adk18613 Anti-huma Adk18815 Anti-huma	Adl25464 Human mAb Aei65125 Anti-Ang-
	7 7 ADK18936 7 8 ADL25456 3 10 AEK98534	6 10 AEI64964 6 10 AEI64968 6 7 ADX18597	۲.	7	10	10 6	2 10 AEG17553 5 7 ADK18778	5 7 ADK18613 5 7 ADK18815	5 8 ADL25464 1 10 AEI65125
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22 5 4 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	24 24 28	29 30 31	32 33	34 35	36 37	8 6 8 7	40 41	42 43	44 45

## ALIGNMENTS

RESULT 1

antiinflammatory; immunomodulator; cytostatic; gene therapy Anti-human PDGF-D antibody protein related sequence #2. ADK18776 standard; protein; 125 AA. 06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860. (first entry) (ABGE-) ABGENIX INC. WO2003057857-A2. Homo sapiens. 06-MAY-2004 17-JUL-2003. ADK18776; ADK18776 

Weber R; Gazit G, Chen F, Yang X, Feng X, Corvalan JRF, Jia X, WPI; 2003-587119/55. Bezabeh B;

growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 200; 255pp; English

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 306641880.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

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                                                                Length 125;
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                                                              Score 672; DB 7;
Pred. No. 3.4e-54;
; Mismatches 0;
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100.0%; Pre
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                                                                                                            Conservative
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                                                                                   Local Similarity
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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY

100.0%; Score 672; DB 7; Length 125; 100.0%; Pred. No. 3.4e-54; tive 0; Mismatches 0; Indels

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ilarity 100.0%; Pred. No. 3.4e-54;
Conservative 0; Mismatches 0;
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Matches 125; Conserv
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antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

Human mAb 6.4 heavy chain variable region protein SEQ ID NO:2.

(first entry)

17-JUN-2004

ADL25392;

nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                          factor-D (PDGF-D), useful for treating chronic and recurrent
diseases, such as inflammation, autoimmunity and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 672; DB 7; Length 125; 100.0%; Pred. No. 3.4e-54; ive 0; Mismatches 0; Indel8
                                                                                                                                               antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                               Gazit G,
                                                                                                                            Anti-human PDGF-D antibody protein related sequence #39
                                                                                                                                                                                                                                                                                             Chen F,
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 237; 255pp; English
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                                                              ADK18813 standard; protein; 125 AA.
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                                                                                                                                                                                                                                06-JAN-2003; 2003WO-US000398
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VTVSS 125
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binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:
(1) a method of detecting nephritis; (2) a method of treating nephritis;
of treating mesangial cell proliferation; and (4) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial cell proliferation. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 672; DB 8;
100.0%; Pred. No. 3.4e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK18614 standard; protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ID ADK1
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Gaps

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9 9

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY QVQLVQSGAEVKKPGASVKVSCKASGYTPTSYDINWVRQATGQGLEWMGWINPNSGNTDY

Best Local Similarity 100. Matches 125; Conservative

61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120 AQKFQGRVTWTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120

VTVSS 125 125

61 121

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VIVSS

121

ADL25392 standard; protein; 125 AA.

RESULT 5 ADL25392 ID ADL2 XX

The present invention describes an antibody or its binding fragment that binds platelet derived growth farce on the control of the control of

Disclosure; SEQ ID NO 2; 115pp; English.

nephritis.

Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating

Lichenstein H;

Larochelle WJ,

Keyt B,

Gazit-Bornstein G,

Floege J,

WPI; 2004-269881/25.

N-PSDB; ADL25391

(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.

16-SEP-2003; 2003WO-US029414. 16-SEP-2002; 2002US-0411137P

WO2004024098-A2 Homo sapiens

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9 9

WO2003057857-A2.

Homo sapiens.

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AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSGYBYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                              Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                 New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                     antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 638; DB 7; Length 125; 94.4%; Pred. No. 4.7e-51; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                              Gazit G,
                                                      Anti-human PDGF-D antibody heavy chain protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-human PDGF-D antibody protein related sequence #5.
                                                                                                                                                                                                                                                                                              Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 38; 255pp; English
                                                                                                                                                                                                                                                                                              Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK18779 standard; protein; 125 AA
                                                                                                                                                                                                                                                                                              Feng X,
                                                                                                                                                                                                       06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                   07-JAN-2002; 2002US-00041860
                            (first entry)
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                                                                                                                                                                                                                                                                                              Jia X,
                                                                                                                                                                                                                                                                                                                                         WPI; 2003-587119/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 125 AA;
                                                                                                                                             WO2003057857-A2.
                                                                                                                                                                                                                                                                                             Corvalan JRF,
                                                                                                                Homo sapiens
                            06-MAY-2004
                                                                                                                                                                            17-JUL-2003
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antiinflammatory; immunomodulator; cytostatic; gene therapy.

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61 AQKFQGRVTWTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                                                                                                                                                                                                                                                                   are useful for
                                                                                                                                                                                                                                                                                                                                                 The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEKZ93 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYGYGYDYYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                                                                                                                                Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                        New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.9%; Score 638; DB 7; Length 125, 94.4%; Pred. No. 4.7e-51;
                                                                                                                                                                                Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human PDGF-D antibody protein related seguence #145.
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                                                                                                                                                                                Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 203; 255pp; English
                                                                                                                                                                                Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK18919 standard; protein; 125 AA.
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                                                                                      06-JAN-2003; 2003WO-US000398.
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                                                                                                                     07-JAN-2002; 2002US-00041860
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Matches 118; Conservative
                                                                                                                                                                                  Jia X,
                                                                                                                                                                                                                             WPI; 2003-587119/55.
                                                                                                                                                    (ABGE-) ABGENIX INC
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                                                                                                                                                                                  Corvalan JRF,
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                                                          17-JUL-2003
                                                                                                                                                                                                  Bezabeh B;
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ADK18919
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(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                        121 VTVSS 125
                                                                                                                                                                                        Sequence 125 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                      The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                             useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 0.99 arising in the conditioned medium obtained when HBK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                               OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                 Gaps
                                         Weber R;
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                                                                                                                                                                                                                                                                                            Score 638; DB 7; Length 125;
Pred. No. 4.7e-51;
3; Mismatches 4; Indels
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                                         Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human PDGF-D antibody protein related sequence #42.
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                                         Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen F,
                                                                                                                                  Disclosure; SEQ ID NO 343; 255pp; English
                                         Yang X,
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07-JAN-2002; 2002US-00041860
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                                         Feng
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.4
Matches 118; Conservative
                                        Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                       WPI; 2003-587119/55.
                    (ABGE-) ABGENIX INC
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                                                                                                                                                                                                                                                                        Sequence 125 AA;
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                                        Corvalan JRF,
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                                                   Bezabeh B;
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                                                                                                                                                                                                            The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEKZ93 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lichenstein H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
growth
human
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New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larochelle WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 638; DB 7;
Pred. No. 4.7e-51;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; human; monoclonal antibody; mAb
                                                                                                                                             Disclosure; SEQ ID NO 240; 255pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL25444 standard; protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floege J, Gazit-Bornstein G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.9%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6-SEP-2003; 2003WO-US029414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.4
Matches 118; Conservative
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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antihiflammatory, dermacological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAA) variable region sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 638; DB 8;
Pred. No. 4.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                   Disclosure; SEQ ID NO 54; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.4
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 125 AA;
  nephritis
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSGYDYYYGMDVWGQGTT 120 **QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY** QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT Gaps ö Length 125; 4; Indels VTVSS 125 VIVSS 125 61 121 121 g 엄 셤 ઠ ò

120

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9 9

> ADK18864 standard; protein; 126 AA. 06-MAY-2004 ADK18864; RESULT 11 ADK18864
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> LID ADKI
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> XX AAC ADK1
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> XXX ADT1
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> XXX

Anti-human PDGF-D antibody protein related sequence #90. (first entry

antiinflammatory; immunomodulator; cytostatic; gene therapy

WO2003057857-A2 Homo sapiens

17-JUL-2003

07-JAN-2002; 2002US-00041860

06-JAN-2003; 2003WO-US000398

(ABGE-) ABGENIX INC

Weber R; Gazit G, Ę, Chen Yang X, Feng X, Corvalan JRF, Jia X, Bezabeh B;

WPI; 2003-587119/55.

growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 288; 255pp; English.

The invention relates to a human monoclonal antibody that binds to

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                                                                                                                                                                                                                                                                                                                                                                         61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGP-D). The antibodies are useful for reacting ofhronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGP-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGP-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
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platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
                                                                   generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT
                                                                                                                                                                                                                                                 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                               Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; immunomodulator; cytostatic; gene therapy.
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                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                           Score 593.5; DB 7;
Pred. No. 6.1e-47;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 19; 255pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK18595 standard; protein; 126 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                             Query Match 88.3%;
Best Local Similarity 89.7%;
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                            125
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                                                                                                                                                                              Sequence 126 AA;
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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                              QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMPNSGNTGY
                                                                                                                            AQKFQGRVTMTRDTS1STAYMBLSSLRSEDTA1YYCVR-GFGYSYNYDYYYGMDVWGQGT
                                                                                                                                       61 AQKFQGRVIMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT
                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                               Gaps
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                                           Length 126;
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                                                                                                                                                                                                                                                                                                                               antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gazit G,
                                                              Indels
 sequence corresponds to a protein used in the invention
                                                                                                                                                                                                                                                                                                          Anti-human PDGF-D antibody protein related sequence
                                         Score 593.5; DB 7;
Pred. No. 6.1e-47;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 201; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang X,
                                                                                                                                                                                                                                            ADK18777 standard; protein; 126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JAN-2002; 2002US-00041860.
                                         88.3%;
                                                                                                                                                                                                                                                                                      (first entry)
                                      Query Match
Best Local Similarity 89.7°
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABGE-) ABGENIX INC.
                                                                                                                                                                     TVTVSS 125
                                                                                                                                                                                       121 TVTVSS 126
                    Seguence 126 AA;
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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

(1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antihilammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                                     AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
                                                                                                                         AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT 120
                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet derived for treating.
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that binds
medicament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an antibody or its binding fragment growth factor-DD (PDGF-DD) for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 18; 115pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-269881/25.
                                                                                                                                                                                                                                                                            TVTVSS 126
                                                                                                                                                                                                                 TVTVSS 125
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Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADL25407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nephritis.
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Gaps

1,

Indels

8

88.3%; Score 593.5; DB 7; 89.7%; Pred. No. 6.1e-47; iive 4; Mismatches 8;

Conservative

Local Similarity

Best Local Sım Matches 113;

Query Match

DB 7; Length 126;

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The new invention relates to a fully human monoclonal antibody or its binding fragment that binds to Ten-M2 and neutralizes Ten-M2 activity. Also described are a method for assaying the level of Ten-M2 in a parient sample; a composition comprising the antibody or its binding fragment and a thiology is a full-length antibody. Alternatively, the human monoclonal antibody that binds to Ten-M2 comprises a heavy chain having an amino acid sequence selected from any of fully defined 116-127 amino acid sequences (SEO ID NO. 2, 6, 10, 14, 18, 22, 26, 30, 34, 34, 24, 46, or 50) given in the specification. It also comprises a light chain having an amino acid sequence selected from any of fully defined 101-113 amino acid and sequence selected from any of fully defined 101-113 amino acid sequences (SEO ID NO. 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, or 50) given in the specification. Alternatively, the antibody or its binding fragment binds to Ten-M2, where the antibody or binding fragment cross-reacts with a fully human anti-Ten-M2 antibody selected from mabl20, Mabl40, and Mabl71, Mabl79, Mabl99, on Mabl23, or an antibody or Ten-M2 in a patient sample comprises contacting the patient sample comprises contacting the patient sample comprises contacting the patient sample. The antibodys and determining the presence or amount of anti-Ten-M2 antibody, and determining the presence or amount of anti-Ten-M2 antibody or Ten-M2, in the patient sample. The antibodies can be used for treating symptoms and conditions associated with Ten-M2 activity, e.g. cancer. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; antibody therapy; Ten-M2; diagnosis; pharmaceutical; tumor; cytostatic; neoplasm; cancer; heavy chain variable region.
                                                                                119
                                                                                                 New fully human monoclonal antibody that binds to Ten-M2 and neutralizes Ten-M2 activity, useful for treating symptoms and conditions associated with Ten-M2 activity, e.g. cancer.
9
                                      9
                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                61 AOKFOGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-Ten-M2 antibody heavy chain variable region, SEQ ID:50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larochelle W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 50; 141pp; English.
                                                                                                                                                                                                                                                                                                       AEK98538 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2005; 2005US-0665592P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2006; 2006WO-US011031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ettenberg S, Masterman S,
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2006-670467/69.
                                                                                                                                                                                           121 TVTVSS 126
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                                                                                                                                                                                                                              61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                              9
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                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
sequence is a human anti-Ten-M2 antibody heavy chain variable region
protein sequence.
                                                                                                                              Gaps
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;
                                                                                          Score 588; DB 10; Length 123;
Pred. No. 1.9e-46;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 25, 2007, 04:05:20 Job time : 109.404 secs
                                                                                             87.5%;
89.6%;
                                                                                                                Best Local Similarity ov.o
Matches 112; Conservative
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                             121 VTVSS 125
                                                                                                                                                                                                                                                                                                                               119 VTVSS 123
                                                               Sequence 123 AA;
                                                                                               Query Match
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 04:05:37 ; Search time 10 Seconds (without alignments) 1261.509 Million cell updates/sec

US-10-665-383-2 672 1 QVQLVQSGAEVKKPGASVKV......YDYYYGMDVWGQGTTVTVSS 125

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

11,1000		*				
No.	Score	Match	Length	DB		Description
н	557	82.	;		834014	g heavy
8	537.5	80.0	136	~	S31600	Ig heavy chain V r
m	534	79.5	129	7	S46393	g heavy
4	516.5		118	7	S36265	g heavy chain V
S	515		123	~	D33548	g heavy
9	514		129	7	S36260	g heav
7	511.5	76.1	135	~	S49530	u
00	510.5	•	132	7	S31596	heav
σ	200		131	7	S26792	heavy
10	499		119	~	PH0961	heavy chain V
11	496.5		110	~	PH1670	heavy
12	496	73.8	96	0	S26918	heavy
13	495.5	73.7	132	N	PH0954	
14			171	~	S23623	heavy
12			118	7	PH1666	heavy
16	493.5		136	~		heavy
17			143	7	EIHUND	heavy
18	488		127	N	PH0955	heavy chain
19	487.5	72.5	124	7	S19665	heavy
50	486		133	~	C33548	þeg
21	486		627	7	S14683	ם
22	484		142	7	A32483	Ig heavy chain V r
23	480	71.4	122	· (2)	S36271	hea
74	480		160	~	PL0105	i-PR2 erythr
25			126	~	B33548	heavy
56			114	N	PH1667	g heavy
27	473.5	70.5	128	~	PH0952	
28		•	120	N	831999	g heavy
29	LO.	é.	109	~	PH1668	g heavy

_	heavy chain	heavy	heavy chain	Ig heavy chain V r	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy chain	heavy chain	heavy	heavy chain
S26938	S31680	S18551	144151	869899	S20783	PH0958	S26912	PH0957	826789	S46394	A33548	PH1669	868170	PH0959	B32274
a	^1	a	N	~	N	N	a	a	~						
	•	• •							CA.	N	~	N	~	7	N
86	117	117	126	104	121	122	86	125							135 2
		•		68.9 104					120	132	129	110	125	116	•
5 69.2		5 69.2	5 69.2		68.8	68.5	68.0	67.9	67.8 120	132	67.6 129	67.3 110	66.8 125	66.7 116	. 66.4

## ALIGNMENTS

RESULT 1 S34014

	Ig heavy chain V region - human
	C;Species: Homo sapiens (man)
	C;Date: 02-Dec-1993 #sequence revision 10-Nov-1995 #text change 16-Aug-1996
	C; Accession: S34014; S30535
	R;Mariette, X.; Tsapis, A.; Brouet, J.C.
	Eur. J. Immunol. 23, 846-851, 1993
	A; Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
	A; Reference number: S34001; MUID:93209281; PMID:7681398
	A; Accession: S34014
	A;Status: preliminary
	A;Molecule type: mRNA
	A;Residues: 1-127 <mar></mar>
_	A; Cross-references: UNIPARC: UP10000176D31; EMBL: Z18321
	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	C; Keywords: heterotetramer; immunoglobulin
	F;15-98/Domain: immunoglobulin homology < IMM>
	Query Match 82.9%; Score 557; DB 2; Length 127;
	Best Local Similarity 82./%; Fred. No. 1.46-42; Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

	_	9
	2; Gaps	SGNTDY
	2;	GWINPN
	Indels	TGQGLEWM
-42;	10;	WVRQA
Best Local Similarity 82.7%; Pred. No. 1.4e-42;	Matches 105; Conservative 10; Mismatches 10; Indels	1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
milarity	Conserva	VQLVQSGAEV
al Si	105;	1
Best Loc	Matches	ò

>	09	118	120
	1 QVQMVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGGGEEMMGMMNPSSGNTGY 60	61 AQKEQGRVIWIRDISISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQG 118	61 AQKFKGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARALSIGVAVIRGYYYALDVWGQG 120
,		61	61
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119 TTVTVSS 125 121 TTVSVSS 127 ò g

RESULT 2

S1600
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S31600
R;Culsiniar, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Ouisiniar, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31505
A,Accession: S31600
A,Accession: S31600
A,Accession: Ulloon
A;Reference mRNA
A;References: UNIPARC:UDI0000116453; EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
76.6%; Score 515; DB 2;
Best Local Similarity 78.6%; Pred. No. 7.2e-39;
Matches 99; Conservative 10; Mismatches 13
                                   Score 516.5; DB 2
Pred. No. 5.1e-39;
                                                                     6; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V-1 region (WIL2) - human
                                 Query Match
Best Local Similarity 80.0%;
Matches 100; Conservative
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UP1000011663A; EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRUTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                      80 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCAR------WRDAFDIWGQGTM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYG----MDVWG 116
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                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                        Length 136;
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A; Status: preliminary; nucleic acid sequence not shown
                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%; Score 534; DB 2;
79.8%; Pred. No. 1.6e-40;
iive 7; Mismatches 15;
                                                      Score 537.5; DB 2
Pred. No. 8.1e-41;
6; Mismatches 7
C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                      80.0%;
                                                                                          Matches 103; Conservative
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KGTTVTVSS 129
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A;Molecule type: DNA
A;Residues: 1-129 <FIG>
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                                                                         Local Similarity
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C;Accession: D33548
R;Kipps, T.J.; Tomhave, B.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expre A;Reference number: A33548; MUD:89345575; PMID:2503826
A;Accession: D33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trai
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
BMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Recession: S36260
A;Status: preliminary; nucleic acid sequence not shown
A;Nolecule type: mRNA
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A;Residues: 1-129 cGRI>
A;Cross-references: UNIPARC;UPI0000118DEB; EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:C,Superfemily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSY-NYDYYYGMDVWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARA---SYCGYDCYYFFDYWGQGT 117
                                                                                                                                                                                                                                                                                                    AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY-----LDYWGQGTL 113
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Homo sapiens (man)
C.Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHWVRQAPQQGLEMMGWINPNSGGTNY
                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINFNSGGTNY
                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                           Gaps
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                                                                       7;
Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-123 < KIP>
A; Cross-references: UNIPARC:UPI0000176909
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                    61 AOKFOGRVTWTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                        ---PAWGQGTM 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSY-----NYDYYYGMDV 114
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIDWVRQATGQGLEMMGWMNPNSGNTGY
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R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26792
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Bxp. Med. 175, 983-991, 1992
A;Title: Evidence to somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
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                                       Indels
                                                                                                                                                                                                                                                                                           Pred. No. 1.9e-38; 6; Mismatches 7;
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74.4%; Score 500; DB 2;
Best Local Similarity 72.5%; Pred. No. 1.6e-37;
Matches 95; Conservative 13; Mismatches 17.
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   79.2%;
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                                       99; Conservative
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Best Local Similarity
Matches 99; Conserv
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A; Residues: 1-131 <MOR>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31596
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <4NAH>
A;Cesidues: 1-135 <4NAH>
A;Cesidues: 1-135 <4NAH>
A;Cross-references: UNIPPRC:UPI00001166FF; EMBL:Z46348; NID:g560839; PIDN:CAA86467.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 849530
R;Mahmoudi, M.; Edwards, J.; Cairns, B.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                               7
                                                                                                                                                                                                                                                                                                                    AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYD---YYYGMDVWG 116
                                                                                                                                                                                                                                                                                                                                                        61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSPGYCSSTSCPYYYYMDVWG 120
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C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                       1 QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                           Gaps
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                                       Length 129;
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                                                                                                           16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                   Score 514; DB 2;
Pred. No. 9.3e-39;
8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 511.5; DB 2
Pred. No. 1.6e-38;
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                                   76.5%;
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                                   Query Match 76.5
Best Local Similarity 78.3
Matches 101; Conservative
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ò Б ò 셤 ጽ 심 F;36-50/Region: framework 2

Length 132

DB 2;

Score 510.5;

76.0%;

Query Match

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Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (Grach, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (Jrile: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from twansference number: S23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI0000115F93; EMBL:X59702; NID:932010; PIDN:CAA42223.1; PID:C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNY-YYYGM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKEQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGF------GYSYNYDYYYGM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Ciscession: Paper-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
Ciscession: PH0954
Rimartin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                1 QVQLVQSGAEVKKFGASVKVSCKASGYTFTSYDINWVRQATGCGLEWMGWMNPNSGNTGY
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A;Cross-references: UNIPARC:UPI0000176CDE
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>
F;15-98/Domain: immunoglobulin homology < IMM>
                                 Indels
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                                                                                                                                                                                                                           61 AQKFQGRVTMTRDISISTAYMELSSLRSEDTAIYYCVR 98
94.9%; Pred. No. 2.8e-37;
tive 3; Mismatches 2;
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                              93; Conservative
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   Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-171 <OLE>
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C;Species: Homo sapiens (man)
C;Date: 3-4-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1670
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Marrial basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID C;Superfamily: immunoglobilin V region; immunoglobulin homology C;Keywords: heteroretramer; immunoglobulin C;Keywords: heteroretramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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R;Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
Mol. Biol. 227, 776-798, 199
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUD:93021117; PMID:1404388
A;Accession: S26918
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTTVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARG-----YYYYYGMDVWGQGTT
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                                                                                                                             Score 499; DB 2; Length 119;
Pred. No. 1.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: B cell
C;Superifanily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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F;51-67/Region: complementarity-determining 2 F;68-98/Region: framework 3 F;99-107/Region: complementarity-determining 3
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                                                                                                                                   74.3%;
79.2%;
                                                                                                                      Query Match
Best Local Similarity 79.2<sup>3</sup>
Matches 99, Conservative
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A;Residues: 1-98 <TOM>
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                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                  Gaps
                                  17;
   DB 2; Length 171;
Query Match 73.7%; Score 495.5; DB 2; Length Best Local Similarity 70.9%; Pred. No. 5.5e-37; Matches 95; Conservative 9; Mismatches 13; Indels
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Gaps 1; 73.6%; Score 494.5; DB 2; Length 118; 80.5%; Pred. No. 4.5e-37; tive 6; Mismatches 16; Indels 1 Query Match
Best Local Similarity 80.53
Matches 95, Conservative

1 AEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKYAQKPQGRV 60 9 AEVIKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQKFQGRV

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69 TMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGTTVTVSS 125 

Search completed: April 25, 2007, 04:06:39 Job time : 9.5339 secs

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RESULT 2
Q9UL94 HUMAN
ID Q9UL94_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKV......YDYYYGMDVWGQGTTVTVSS
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QEPGB9 HUMAN

QEBJZ2 RAT

Q7Z7P5_HUMAN

Q9UL89_HUMAN

Q924R4_MOUSE

Q524R4_MOUSE

Q528R2_HUMAN

Q4KML5_MOUSE

Q568R2_HUMAN

Q60095_HUMAN

Q60095_HUMAN
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C8_HUMAN
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O8WY24_HUMAN
O9BRV0_HUMAN
O6N030_HUMAN
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Q6N091_HUMAN
HV1G_HÜMAN
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Q9UL94_HUMAN
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Q9QXE9 MOUSE
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMMWRQAPGQGPEMMGVINPSGGSARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Q924q6
P01756
Q924q3
Q924x1
P01747
Q569w9
Q924q5
Q8VCX7
Q65zr6
Q924q9
Q924q9
Q924q9
Q924q9
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSSP; CURRO7110; Ig-like.
InterPro; IRR07110; Ig-like.
InterPro; IRR031399; Ig_sub.
InterPro; IRR03399; Ig_V*set.
InterPro; IRR03396; Ig_V*set.
InterPro; IRR03396; Ig_V*set.
SMART; SM0409; IG, 1.
SMART; SM0409; IG, 1.
SMART; SM0409; IGV 1.
IGV 1.
IGW100310bulin domain.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
18-APR-2006, entry version 21.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                   PRT; 159 AA.
Q924Q6_MOUSE
HV12_MOUSE
Q924Q3_MOUSE
Q924R1_MOUSE
HV03_MOUSE
                                                                            0569W9 MOUSE
0924R3 MOUSE
0924R3 MOUSE
08VCX7 MOUSE
065ZR6 MOUSE
                                                                                                                                                                                Q568Y0_RAT
Q924R0_MOUSE
Q6PJB2_MOUSE
                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY039025; AAK82649.1; -; mRNA.
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61.6
61.6
61.5
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60.0
60.0
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119 AA.

PRT;

fetus."

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61 AOKFOGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE=97362799; Pubmed=9219263; DOI=10.1038/nbt0797-629;
MCONTERMENT R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-611(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Indels
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125 AA; 13516 MW; 0D3CD5C23248BEAC CRC64;
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11-OCT-2004, sequence version 1.
18-APR-2006, entry version 10.
18-ABR-2006, entry version 10.
Name=scFv;
                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                               HSSP, P01751; INQB.
SNR; Q9UL951; 11QB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-sub.
InterPro; IPR013106; Ig-V set.
InterPro; IPR013596; Ig-V set.
Eam; PF07686; V-set; I.
SNART; SN00409; IG; I.
PROSITE; PS50835; IG IIKE; I.
Immunoglobulin domain.
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InterPro; IPR007110; Ig-like.
InterPro; IPR001359; Ig-aub.
InterPro; IPR013106; Ig-V.set.
InterPro; IPR003596; Ig-V.set_sub.
Pfam; PR00468; V.set, 2.
SWART; SM00409; IG; 2.
                                                                                                                                                                                                                     EMBL; AF035019; AAD56255.1; -; mRNA.
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NCBI TaxID=9606;
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Matches 95; Conservative
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SEQUENCE
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01-MAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
Homo sapiens (Human).
                                   01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18.APR-2006, entry version 2.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
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                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorthini;
Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; Pubmed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 494; DB 2; Length 119; 76.0%; Pred. No. 1.7e-41; rive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 119
119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00110; Ig-like.
InterPro; IPR001599; Ig_sub.
InterPro; IPR01106; Ig_Vset.
InterPro; IPR0130596; Ig_Vset.
InterPro; IPR001596; Ig_Vset.
Pfam; PF07686; V-set; I.
SMART; SM00409; IG; I.
PROSITE; PS50835; IG_IKE; I.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035020; AAD56256.1; -; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95; Conservative
                                                                                                                                                              Homo sapiens (Human).
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SMR; Q9UL94; 1-116
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                                                                                                                                                          61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
                                                                                                                                                                        61 AQRFQGRVTWTRDTSISAAYMEVSRLRSDDTAVYYCAREGTGSA----1YGMDVWGQGT 115
                                                                                                                                   9
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                                                                                                                        1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEMMGWIDPNNGDTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bennich H.E., Johansson S.G.O., von Bahr-Lindstrom H.; (In) Bach M.K. (eds.); Immediate hypersensitivity: modern concepts and developments, pp.1-36, marcel Dekker, New York (1978).
                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                    6; Gaps
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Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;
Ell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0005576; C: extracellular region; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0003855; P: immune response; NAS.
InterPro; IPR003599; Ig_sub.
InterPro; IPR003599; Ig_wb.
InterPro; IPR003599; Ig_wb.
InterPro; IPR003596; Ig_V-set_sub.
SWART; SW00406; IGV: 1.
PROSITE; PSS0835; IG_LIKE; 1.
IPROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.
                                                          73.1%; Score 491; DB 2; Length 244; 75.4%; Pred. No. 7.5e-41; ive 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V-I region /FIId=PRO_0000015246.
                                   244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                    21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 0-10-EC-2006, sequence version 2. 30-MAY-2006, entry version 47. 1g heavy chain V-I region ND precursor (Fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 20-147
                                                                                  95; Conservative
                                                                                                                                                                                                                                                                                               STANDARD;
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Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                           120 TVTVSS 125
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                                                                                                                                                                                                                                  116 LVTVSS 121
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                                                                        Best Local Similarity
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61 AOKFOGRVIMIRDISISIAYMELSSLRSEDIAIYYCVRG---FGYSYNYDYYYGMDVWGQ 117
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immnoglobulin heavy chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                  20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Mux X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 124;
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                                                                                                                                          16496 MW; 948F9F72A5366C20 CRC64;
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124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                 T -> V (in Ref. 2).

IH -> HI (in Ref. 2).

VG -> GV (in Ref. 2).

Missing (in Ref. 2).
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76.0%; Pred. No. 3.1e-40;
iive 9; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
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HSSP; P01751; 1NQB.
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Interpro; IPR003599; Ig sub.
Interpro; IPR013106; IgV-set.
Interpro; IPR03596; IgV-set.sub.
Pfam; PF07686; V-set; 1
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QSUL92;
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SMARI; SM0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
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Best Local Similarity 76.0°
Matches 95; Conservative
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AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                           61 AQKEQGRVTMTRDTSTSTVYWELSSLRSEDTAVYYCARGL-YVVVPAAFSRFDYWGQGTL 119
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The German Human cDNA Consortium; Oustka A., Albert R., Mochanyer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bamamalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQÜENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;
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SMART; SM00407; IGc1; 2.
SMART; SM00406; IGc1; 2.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG-MHC; UNKNOWN 2.
PROSITE; PS00290; IG-MHC; IMMUNOGlobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, sequence version 1.
18-APR-2006, entry version 13.
Hypothetical protein DKFZp686016217 (Pragment)
Name-DKFZp686016217;
                                                                                                                                                                                                                                                                                                              05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWBL; BX640710; CAE45829.1; -; mRNA. HSSP; P0175.; 1A6W.
ENR; Q6N041; 268-476.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1-set.
InterPro; IPR003599; Ig_Mb.
InterPro; IPR003599; Ig_Wb.
InterPro; IPR003596; Ig_W-set.
InterPro; IPR013106; Ig_V-set.
Fam; PF07654; C1-set.2.
Pfam; PF07666; V-set; 1.
                                                                                                                                                                                                                                                               PRT;
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Best Local Similarity
                                                                                                                                          VTVSS 124
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OGNO41HU

OGNO41HU

DGNO40HU

DT 05-J

DT 05-J

DT 05-J

DT 18-N

DR Hypo

OC Catam

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RESULT 8

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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-----GFGYSYNYDYYYGMDVW 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF283666; AAL36987.1; -; mRNA.

R SMR; O8W124; 267-410W0.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019883; P:antigen processing, endogenous antigen; IEA.

GO; GO:0019883; P:antigen processing, endogenous antigen; IEA.

R GO; GO:0019883; P:antigen processing, endogenous antigen via . .;

R InterPro; IPR00310; Ig-1ike.

R InterPro; IPR003599; Ig_Cl-set.

R InterPro; IPR003599; Ig_Cl-set.

R InterPro; IPR03599; Ig_Sub.

R InterPro; IPR03599; Ig_V-set.

R InterPro; IPR03599; Ig_V-set.

R InterPro; IPR03596; Ig_V-set.

R Pfam; PF07654; Cl-set; 1.

R Pfam; PF07654; Cl-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.

Submits G., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major

histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                      Demonstrate de la constanta de
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 497 AA: 53666 MW; P24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.5%; Score 474; DB 2; 70.0%; Pred. No. 8.6e-39; cive 13; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001, integrated into UniProtKB/TrEMBL. 01-JUN-2001, sequence version 1. 25-JUL-2006, entry version 36.
                                                                                             01-MAR-2002, integrated into UniProtKB/TrEMBL.
01-MAR-2002, sequence veraion 1.
12-UN-2006, entry version 25.
SNC66 protein.
     497 AA.
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Q9BRVO;
PRT;
QBWY24_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%
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SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GOGTTVTVSS 125
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                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGHAl protein.
Name=IGHAl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BRV0
1D Q9
AC Q9
DT 01
DT 25
DE 1G
GN NA
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80 SQKFQGRVTITRDIWTTTAYMDLSSLRSEDTAVYWCARDAPQGVTTTYF---DYWGQGTL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches
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InterPro; IPR00310; Ig-11ke.
InterPro; IPR003509; Ig-C1-set.
InterPro; IPR003599; Ig-sub.
InterPro; IPR013106; Ig-NHC.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR013106; Ig-V-set.
PEam; PP07654; C1-set; 3.
Pfam; PP07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004, sequence version 1.
27-JUN-2006, entry version 19.
Hypothetical protein DKFZp686115212.
Name=DKFZp686115212,
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BX640724; CAE45841.1; -; mRNA.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Rectum tumor;
The German cDNA Consortium;
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nes 89; Conservative
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SMART; SM00407; IGC1; 2
SMART; SM00406; IGv; 1.
                                                                                                                          GTTVTVSS 125
                                                                                                                                                                                                  GTTVTVSS 147
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                                                                                                                          118
                                                                                                                                                                                                  140
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HUMAN
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Matches
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RR 1875 FOLGA'S 1000.

RR 20,000(0130076; Homo sapiens.

R 20,000(01310076; Homo sapiens.

R 20,000(01201; C:integral to membrane; IEA.

R 20,000(0130106; F:MHC class I receptor activity; IEA.

R 11terPro; IPR001151; Ig-like.

R 11terPro; IPR001597; Ig-Like.

R 11terPro; IPR001309; Ig-MHC.

R 11terPro; IPR001306; Ig-W-set.

R 11terPro; IPR0013106; Ig-V-set.

R 100047; Ig; I.
                                                                                                                                                                                                                     TISSUE-Proteate:

(TISSUE-Proteate:

(TISSUE-Protea
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGc1; 2.
PROSITE; PSC0035; IG LIKE; 4.
PROSITE; PSC00290; IG MHC; UNKNOWN 1.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC005951; AAH05951.1; -; mRNA.
HSSP; P01876; 10W0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Conservative
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGC Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVHLVQSGAEVKKPGASVKVSCTASGYPFTNHFINWVRQAPGQSLEWMWINTGNGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LinkHub; Q6N030; -.. GO; GO: 0016622; C: integral to membrane; IEA.
GO; GO: 0016622; C: membrane; IEA.
GO; GO: 00301.06; F: MHC class I receptor activity; IEA.
GO; GO: 0019883; P: antigen presentation, endogenous antigen; IEA.
GO; GO: 0019885; P: antigen processing, endogenous antigen via.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
PROSITE; PS000835; IG LIKE; 4.
PROSITE; PS00290 : IG MAC; UNKNOWN 2.
Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.1%; Score 457.5; DB 2; Length 71.2%; Pred. No. 4.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 AA; 57020 MW; 93B5F98613BF6382 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  HSPP; P01751; 1A6W.
HSSP; P01751; 1A6W.
SMR; Q6N091; 270-478
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1-set.
InterPro; IPR003599; Ig_whc.
InterPro; IPR003599; Ig_wb.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set.
                                                                                                                                                                                                                                                                                                EMBL; BX640625; CAE45779.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP07654; C1-8et; 2. Pfam; PP07686; V-8et; 1. SWART; SM00409; IG; 1. SMART; SM00407; IG; 2. SMART; SM00406; IGV; 1.
Homo sapiens (Human)
                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TVTVSS 125
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                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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HV1G_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NQKFKDRVIMITIDKSFSTAYMDLRSLRSADSAVYYCAR-----YYDDHYCLDYWGQGTT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                      01-MAR-2001, sequence version 1.
18-APR-2006, entry version 22.
Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                      Song X.T., Feng Z.Q., Guan X.H.; "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.7%; Score 455; DB 2;
69.6%; Pred. No. 1.4e-37;
iive 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 18-APR-2006, entry version 13. Hypothetical protein DKFZp686C02220 (Fragment).
                                                                                                                                                                                      01-MAR-2001, integrated into UniProtKB/TrEMBL.
                                                                                                                                                  119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF282622; AAG01452.1; -; mRNA.
HSSP; P01751; 1A6W.
SMR; Q9GYZ2; 1-119.
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001110; Ig-like.
InterPro; IPR03599; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR03596; Ig_V-set_sub.
Pfam; PP07686; V-set_il.
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                     VTVSS 125
                                                       137 VTVSS 141
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                  Q9GYZ2_MOUSE
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Q6N091;
                     121
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Hypothetical protein Name=DKFZp686C02220;

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RESULT 12

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61 AQKFQCRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGY-SYNYDYYYGMDVWGQGT 119
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
TISSUB=Human rectum tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVIG HUMAN STANDARD; PRT; 117 AA. P23083; 01-NOV-1991, integrated into UniProtKB/Swiss-Prot. 01-NOV-1991, sequence version 1. 30-MAY-2006, entry version 38. Ig heavy chain V-I region V35 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.4%; Score 446; DB 2; Best Local Similarity 69.8%; Pred. No. 5.7e-36; Matches 88; Conservative 12; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy-chain locus.";
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                  Local Similarity 85.7 es 84; Conservative
                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                      >117
                                                HSSP; P01751; 1NQB.
SMR; P01743; 20-117.
LinkHub; P01743; -.
                                    PIR; A02024; HVHUHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
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Matches
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                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                Mariette X., Tsapis A., Brouet J.C.; "Nucleotidic sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
21-JUL-1986, sequence version 1.
30-MAY-2006, entry version 43.
Ig heavy chain V-I region HG3 precursor.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Buarchontoglires; Primates, Haplorrhin;
                                                                                             Eur. J. Immunol. 23:846-851(1993).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65:6%; Score 441; DB 1; Length 117; 85.7%; Pred. No. 3.5e-36; ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V-I region V35./FTId=PRO_000015245.
                                                                                                                                                                                                                                                 GO; 00:005576; C:extracellular region; NAS.
GO; 00:003823; F:antigen binding; NAS.
GO; 00:006955; P:immune response; NAS.
InterPro; IPR013106; Ig-like.
InterPro; IPR013106; Ig-set.
InterPro; IPR013596; Ig-set.
SMART; SM00406; Igv. set.
InterPro; IPR013106; Ig V-set.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR 98
                                                                                                                                                                         EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA.
PIR; S00476; HVHU35.
HSSP; P01751; NUS.
SMR; P21083; 20-117.
Ensembl; ENSG0000130076; Homo sapiens.
                        NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
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                                    MEDLINE=93209281; PubMed=7681398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae; Homo.
EMBO J. 7:1047-1051 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              117
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                                                                                                                                                                                                                                         P23083; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                    glycoprotein.
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                                                                                                                                                                                                                                          LinkHub;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg Kl., Feingold E.A., Grouse L.H., Derge J.G., Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domai\overline{\mathbf{n}}_i; Immunoglobulin V region; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AOKFOGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%; Score 440; DB 1;
85.7%; Pred. No. 4.4e-36;
                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR07110; IG-like.
InterPro; IPR07110; IG-like.
InterPro; IPR03596; Ig-V-set.
Fam; PF07686; V-set; I-SMART; SM04406; IGY; I-SMART; SM04406; IGY; I-SMART; PS50835; IG-LIKE; I-SMART; PSF0868; IG-LIKE; I-SMART; PSF0868; IG-LIKE; I-SMART; PSF08935; IG-LIKE; I-SMART; PSF08955; I-SMART; PSF08955; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-07L-2004, integrated into UniProtKB/TrEMBL. 05-07L-2004, sequence version 1. 27-07N-2006, entry version 21. Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 AA
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EMBL; J00240; AAA52988.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-Noberivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                              EMBL; BC065733; AAH65733.1; -; mRNA.

RSP; P01751; 1A6W.

ROW, GOF0091, 250-45W.

ROY, GO:0016021; C:integral to membrane; IEA.

ROY, GO:0016020; C:membrane; IEA.

ROY, GO:0010803; P:antigen presentation, endogenous antigen yie interpre; IPR007110; Ig-like.

RICTOR GO: GO:0019885; P:antigen presentation, endogenous antigen yie interpre; IPR003100; Ig-like.

RICTOR GO: GO:0019885; P:antigen presentation, endogenous antigen yie interpre; IPR003506; Ig-like.

RICTOR GO: GO:0019885; P:antigen presentation, endogenous antigen yie interpre; IPR003506; Ig-like.

RICTOR GO: GO:0019885; P:antigen presentation, endogenous antigen yie interpre; IPR003506; Ig-like.

RICTOR GO: GO:0019885; F:antigen presentation, endogenous antigen yie interpre; IPR003506; Ig-like.

RICTOR GO: GO:0019885; F:antigen present; F:antigen yie interpre; IPR003506; Ig-like.

RICTOR GO: GO:0019885; F:antigen present; F:antigen yie interpre; ROWO407; IG: 1.

RWART; SM00406; IG: 1.

RWART; SM00406; IG: 1.

RROSITE; PS002905; IG-MHC; UNKNOWN 2.

RROSITE; PS002905; IG-MHC; UNKNOWN 2.
                                                                                                                           -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.2%; Score 438; DB 2; Length 480; 68.5%; Pred. No. 3.4e-35; rive 13; Mismatches 19; Indels
                                                                             Strausberg R.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 AA; 51998 MW; 2E286C57E4F0ED65 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                       NUCLEOTIDE SEQUENCE.
TISSUE-Glandular pool- thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 68.5%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fransmembrane
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Db 134 TLVTVSS 140 Search completed: April 25, 2007, 04:06:35 Job time : 85.0989 secs

119 TTVTVSS 125

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음 &

20 QVQLVQSGAEVKKTGASVKVSCKASGYSISDNYIHWVRQAPGQGLEMMAMIRPQNGGTVS 79

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Query Match
Best Local Similarity
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US-09-025-769B-36
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36, Appl
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696.311 Million cell updates/sec
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Sequence 22,
Sequence 22,
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Sequence 22,
Sequence 28,
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Sequence 59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/iaa/HCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                672
1 QVQLVQSGAEVKKPGASVKV.....YDYYYGMDVWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                      April 25, 2007, 04:06:51 ; Search time 16 Seconds
version 6.2.1 - 2007 Biocceleration Ltd.
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US-08-472-281A-94
US-08-472-281A-94
US-09-462-140D-102
US-09-462-140D-102
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US-09-025-769B-59
US-09-020-70A-36
US-09-490-153-36
US-09-490-153-59
US-09-490-153-59
US-09-490-153-59
US-09-490-324-59
US-09-490-324-59
US-09-490-153-22
US-09-490-153-22
US-09-490-153-22
US-09-490-153-22
US-09-490-153-22
US-09-199-149-3
US-09-199-149-3
US-08-561-521-45
US-08-561-521-45
US-08-561-521-45
US-08-561-521-45
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US-08-561-521-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650591 seqs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
  GenCore (c) 1993 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                             Copyright
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                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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27 501 74.6 119 5 PCT-US95-01219-10 Sequence 10, Appl 29 74.1 119 2 US-09-438-954-41 Sequence 41, Appl 30 496 73.8 117 2 US-09-515-697-96 Sequence 96, Appl 31 493.5 73.4 139 1 US-08-255-97-96 Sequence 19, Appl 32 493.5 73.4 139 1 US-08-603-024-18 Sequence 19, Appl 34 493.5 73.4 139 2 US-08-603-024-18 Sequence 19, Appl 34 493.5 73.4 139 2 US-08-603-024-18 Sequence 19, Appl 36 487 72.5 118 3 US-08-85-809-14 Sequence 13, Appl 37 12.5 12 US-08-95-080-14 Sequence 13, Appl 37 12.5 12 US-08-95-080-14 Sequence 23, Appl 39 487 72.5 121 2 US-08-96-609-23 Sequence 23, Appl 40 72.5 121 2 US-08-96-690-23 Sequence 23, Appl 40 72.5 121 2 US-08-96-690-23 Sequence 23, Appl 40 72.5 121 2 US-08-561-521-12 Sequence 24 Appl 41 71.6 123 1 US-08-482-882-86 Sequence 86, Appl 44 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 44 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 44 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 44 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 44 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 123 1 US-08-487-1130-86 Sequence 86, Appl 45 481 71.6 US-08-487-1130-86 Sequence 86,
74.6 119 5 PCT-US95-01219-10 74.1 119 2 US-09-438-954-41 73.8 117 2 US-09-515-697-96 73.4 139 1 US-08-553-877(-19 73.4 139 1 US-08-853-877(-19 73.4 139 2 US-08-63-024-18 73.4 139 2 US-08-63-024-18 73.5 118 3 US-08-650-204-14 72.5 121 1 US-08-675-221B-13 72.5 121 1 US-08-964-690-23 72.5 121 2 US-08-964-690-23 72.5 121 2 US-08-964-690-23 72.5 121 2 US-08-964-690-23 72.5 121 2 US-08-964-690-23 72.5 121 1 US-08-86-86 72.6 123 1 US-08-482-86 73.6 123 1 US-08-487-113D-86 74.6 123 1 US-08-487-113D-86 74.6 123 1 US-08-487-113D-86 75.7 1 US-08-487-113D-86
74.6 74.6 73.8 73.8 117 2 73.8 117 2 73.4 73.4 73.4 73.5 72.5 118 3 72.5 72.5 121 2 72.5 121 2 72.5 121 2 72.5 121 2 72.5 72.5 72.5 72.5 72.5 72.5 72.5 72.
444.6 44.6 733.8 733.8 732.5 722.5 722.5 72.6 72.6 72.6 72.6 72.6 72.6 72.6 72.6
444.6 44.6 733.8 733.8 732.5 722.5 722.5 72.6 72.6 72.6 72.6 72.6 72.6 72.6 72.6
224 229 230 331 332 44996 332 44993 44993 531 5493
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

TOPOLOGY: linear
MOLECULE TYPE: protein
JS-09-025-769B-36
Query Match
Bost Local Similarity 84.0%; Pred. No. 1.9e-44;

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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AQKFQGRVTWTRDTSISTAYMELSSLRSEDTAVYYCARWGG-----DGFYAMDYWGQGTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKRGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                            Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 1.9e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
PILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: Colin G. SENDERCCOCK, ESG.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 912-2000
TELEPRORE: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-070A-36
                                                                                                                           US-09-490-070A-36; Sequence 36, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                             APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS
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84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 84.0 Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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121 VTVSS 125
                                        116 VTVSS 120
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US-09-490-070A-59
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                                                                                                           RESULT 3
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                                                                                                                               61 AOKFOGRVTMTRDISISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                     61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCARWGG-----DGFYAMDYWGQGTL 115
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                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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  Gaps
2;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                        Sequence 59 Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCES.
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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84.0%; Pred. No. 1.9e-
:ive 5; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPHUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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Matches 105; Conservative
  Matches 105; Conservative
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SEQUENCE CHARACTERISTICS
                                                                                                                                                    STATE: New York COUNTRY: USA
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                                                                                                                                                                                                                                                        ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 120;
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                                                                                                                                                Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.6%; Score 541.5; DB 2; Best Local Similarity 84.0%; Pred. No. 1.9e-44; Matches 105; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/490,070A
PILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/ABENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                 STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-070A-59
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US-09-490-153-36
; Sequence 36, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Rnappik, Pack
; Ilag, Vic
; Ge, Liming
Moroney, Simon
Sequence 59, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: D.C.
COUNTRY: USA
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Matches 105; Conservative
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                  ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRICA APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1996
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 596-9000
TELEFRAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

80.6%; Score 541.5; DB 2
Best Local Similarity 84.0%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-153-36
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWYRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
G, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 541.5; DB 2
Pred. No. 1.9e-44;
5; Mismatches 10
                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)596-90
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.6%;
Best Local Similarity 84.0%;
Matches 105; Conservative 5
                                ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 VTVSS 120
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US-09-490-324-36
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61 AQKFQGRVTMTRDISISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OVOLVOSGABVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Moroney, Simon
Plucekthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
  PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 1.9e-44;
5; Mismatches 10;
                                                                      FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-324-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/09490324 Patent No. 6828422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.6%;
Best Local Similarity 84.0%;
Matches 105; Conservative
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKEQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCARWGG-----DGFYAMDYWGQGTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWYRQAPGQGLEMMGWINPNSGGTNY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 541.5; DB 2; Length 120;
Pred. No. 1.9e-44;
5; Mismatches 10; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
ITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                 REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELICATION UNMER: US/09/025,769B
PILING DATE: 18-FEB-1996
PRIOR APPLICATION DATA:
PPLICATION NUMBER: EP 95 11 3021,0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                      NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-490-124-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09025769B Patent No. 6300064
                                                                                                                                                                               TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                   LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                   TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                       80.6%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 VTVSS 120
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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61 AOKEOGRVTMTRDISISTAYMELSSLRSEDTALYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                      Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Bhrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                  Query Match 78.6%; Score 528; DB 2; L
Best Local Similarity 82.5%; Pred. No. 3.5e-43;
Matches 104; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
INFORMATION FOR SEQ ID NO: 22 SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                            LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: protein US-09-025-769B-22
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61 AQKFQGRVTWTKDTSISTAYMELSSLRSDDTAVYYCARDGDG-------GFDYWGQGT 111
                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                        1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENTE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.6%; Score 528; DB 2; L. Best Local Similarity 82.5%; Pred. No. 3.5e-43; Matches 104; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 22:
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  Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                  120 TVTVSS 125
                                                                                                                                                                                                                                                                           112 LVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                        US-09-490-324-22
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                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYCARDGDG-------GFDYWGQGT 111
                                                                                                                                                                                                                                                                               61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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                                                                                                                                                                                                               1 QVQLVQSGAEVKKRGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                          Gaps
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
RAPPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                          Query Match 78.6%; Score 528; DB 2; Length 117; Best Local Similarity 82.5%; Pred. No. 3.5e-43; Matches 104; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 528; DB 2; Length 117;
Pred. No. 3.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATTON:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-070A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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82.5%;
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Best Local Similarity
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Best Local Similarity
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US-09-490-153-22
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APPLICANT: Texuli, Takashi
APPLICANT: Texuli, Takashi
APPLICANT: Texuli, No. 6803039uaki
APPLICANT: Hori, No. 6803039uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN MONOCLONAL USB THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USB THEREOF
TITLE OF INVENTION: PHARMACEUTICAL USB THEREOF
TITLE OF INVENTION: PARAMACEUTICAL USB THEREOF
TITLE OF INVENTION: PARAMACEUTICAL USB THEREOF
TITLE OF INVENTION: PARAMACEUTICAL USB THEREOF
THERE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR PELLING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
61 AQKRQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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; Pred. No. 2.6e-42;
10; Mismatches 16; Indels
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Patent No. 6160099;
GENERAL INFORMATION:
APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Trulli Jr., Stephen H.
TILE REPERENCE: P60860
CURRENT APPLICATION NUMBER: US/09/199,149;
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37;
SEQ ID NO 3;
SEQ ID NO 3:
SEQ ID NO 3:
CURRENT PATENT NOS: 37
                           61 AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARDGDG-
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Patent No. 6803039
GENERAL INFORMATION:
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79.2%;
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TYPE: PRT
CRGANISM: Kabat VH subgroup I
US-09-149-149-3
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Best Local Similarity 79.2.
Thea 99; Conservative
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US-09-859-053-28
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US-09-859-053-28
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LENGTH: 470
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61 AOKFOGRVTMTRDTSISTAYMELSSIRSEDTAIYYCVR-GFGYS---YNYDYYYGMDVWG 116
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                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINP-GGDTNY
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                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
Query Match 76.3%; Score 513; DB 2; Length 125; Best Local Similarity 80.6%; Pred. No. 1e-41; Matches 104; Conservative 8; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.0%; Score 510.5; DB 1; Best Local Similarity 77.9%; Pred. No. 1.8e-41; Matches 102; Conservative 7; Mismatches 13;
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CTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08202047 Patent No. 5800815 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                 117 QGTTVTVSS 125
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STRANDEDNESS: si:
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        Qy
        60 YAQKFQGRVTWTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYS-----YNYDYYYGMDV 114

        Db
        61 YAQKFQGRVTITADTSISTAYMELSSLRSEDTAVYYCARAPGYGSGGGCYRGDYF---DY 117

        Qy
        115 WGQCTTVTVSS 125

        Db
        118 WGQCTLVTVSS 128
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Search completed: April 25, 2007, 04:08:31 Job time: 16.7133 secs

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Sequence 230, App
Sequence 372, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 38, Appli
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240, App
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119, App
121, App
1349, App
144, App
146, App
146, App
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Copyright (c) 1993 - 2007 Biocceleration Ltd
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Sequence 125, App
Sequence 61, Appl
Sequence 37, Appl
Sequence 302, App
Sequence 29, Appl
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Sequence 29, Appl
Sequence 162, Appl
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Sequence 101, Appl
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Sequence 103, Appl
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Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Yang, Xiao-Dong

APPLICANT: Tang, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

TITLE OF INVENTION: ATHEROPE

FILE REFERENCE: AGGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

NUMBER OF SEQ ID NOS: 377
              US-10-665-380-22
US-10-309-762-125
US-10-269-805-61
US-10-041-860-37
US-10-041-860-239
US-10-041-860-239
US-10-65-333-74
US-10-721-763-29
US-10-721-763-29
US-10-731-763-29
US-10-731-763-29
US-10-731-763-29
US-10-731-763-29
US-10-731-763-29
US-10-731-763-102
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US-10-731-763-102
US-10-731-763-103
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APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 100.
Matches 125; Conservative
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US-10-041-860-48
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Sequence 372, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
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ORGANISM: homo sapiens
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ORGANISM: homo sapiens
US-10-665-383-2
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LENGTH: 125
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                                   APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGGINX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PASSES for Windows Version 4.0
SEQ ID NO 2.00
LENGTH: 125
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Publication No. US20030157109A1
GENERAL INFORMATION:
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Tang, Xiao
APPLICANT: Chen, Francine
APPLICANT: Ghen, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
                     ang, Xiao-Dong
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ORGANISM: homo sapiens
US-10-041-860-200
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ORGANISM: homo sapiens
Feng, Xiao
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Best Local Similarity
Matches 125; Conserv
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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; Sequence 2, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: LaRochelle, William
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: WISING ANTI-PDGF-DD ANTIBODIES
; TITLE OF INVENTION: NUMBER: 06/411,137
; CURRENT FILING DATE: 2003-09-16
; PRIOR PAPLICANION NUMBER: 60/411,137
; SOFTWARE: FastESQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 125
; TUDE FROME F
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100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels
SENERAL INCOCATALON:
APPLICANT: Corvalido:
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ATHEREOF
FILE OF INVENTION: THEREOF
FILE SERERENCE: AGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PASTSEQ for Windows Version 4.0
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121 VTVSS 125
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                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
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                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                        Gaps
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    Length 125;
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APPLICANT: Chen, Raco-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFRENCE: ABGENTA: 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.9%; Score 63%; DB 4; Length 125; 94.4%; Pred. No. 1.2e-50; ive 3; Mismatches 4; Indels
                                        Indels
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100.0%; Score 672; DB 4;
100.0%; Pred. No. 9.5e-54;
iive 0; Mismatches 0;
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US-10-041-860-203
US-10-041-860-203

**Sequence 203, Application US/10041860

**Publication No. US20303157109A1

**GENBRAL INFORMATION:

**APPLICANT: Corvalan, Jose R.F.

**APPLICANT: Feng, Xiao-Chi

**APPLICANT: Feng, Xiao-Dong

**APPLICANT: Yang, Xiao-Dong

**APPLICANT: Gazit, Gadi

**APPLICANT: Weber, Richard
                                                                                                                                                                                                                                                                                                                                                   US-10-041-860-38
; Sequence 38, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
  Query Match 100.
Best Local Similarity 100.
Matches 125; Conservative
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Best Local Similarity
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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US-10-041-860-240

Sequence 240, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Yang, Xiao-Chi

APPLICANT: Yang, Xiao-Chi

APPLICANT: Yang, Xiao-Chi

APPLICANT: Gazit, Gadi

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX: 051A

CURRENT APPLICATE: ABGENIX: 051A

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

ELENGTH: 125

TURE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX: 051A

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

EBROGHE: 125

TUPE: PUBLICANT: 
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Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT PELING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 125
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Matches 118; Conservative
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ORGANISM: homo sapiens
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CORGANISM: homo sapiens
US-10-041-860-240
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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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US-10-041-860-19
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APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: Keyt, Bruce
APPLICANT: LaRochelle, William
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WETHOO FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: WETHOO FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REFERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT APPLICATION NUMBER: 60/411,137
PRIOR FILING DATE: 2003-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FREESEQ for Mindows Version 4.0
SEQ ID NO 54
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.9%; Score 638; DB 4; Length 125; Best Local Similarity 94.4%; Pred. No. 1.2e-50; Matches 118; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%; Score 638; DB 4; Length 125; 94.4%; Pred. No. 1.2e-50; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF PILE REFERENCE: ABGENIX.051A CURRENT APPLICATION NUMBER: US/10/041,860 NUMBER FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: PSELESEQ for Windows Version 4.0
                                                         Application US/10041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 54, Application US/10665383 ; Publication No. US20040141969A1
                                                                                                               APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Ghen, Francine
APPLICANT: Ghen, Francine
APPLICANT: Bezabeh, Binyam
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                                                                               US20030157109A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343
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US-10-665-383-54
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Matches 118; Conserv
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                                                             Sequence 343, Applic Publication No. US20 GENERAL INFORMATION:
                                           JS-10-041-860-343
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 343
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US-10-665-383-54
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61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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                                                                           61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                     61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYGYDYYYGMDVWGQGTT 120
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APPLICANT: Peng, Xiao-Dong
APPLICANT: Then, Francine
APPLICANT: Gazir, Gadi
APPLICANT: Gazir, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/10/041,860
CURRENT APLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 126
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APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
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Pred. No. 1.5e-46;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.3%;
Best Local Similarity 89.7%;
Matches 113; Conservative
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Concerning of the control 
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ORGANISM: homo sapiens
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GENERAL INFORMATION:

APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Gazit, Gadi
APPLICANT: Reserve Francine
APPLICANT: Reserve Francine
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SEQ TYARRE: PSELSEQ for Windows Version 4.0
SEQ ID NO 201
LENGTH: 126
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Publication No. US20030157109A1
GENERAL INFORMATION:
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Matches 113, Conservative
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US-10-041-860-201
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US-10-041-860-288
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1.
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86.2%; Score 579.5; DB 4; Length 125;
Best Local Similarity 89.4%; Pred. No. 2.7e-45;
Matches 110; Conservative 4; Mismatches 8; Indels 1.
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Reyt, Bruce
APPLICANT: LaRochalle, William
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WETHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: WESTHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: WISHOD ANTIBODIES
FILE REFERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2003-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Tolid, Xiao-Chi
APPLICANT: Fend, Xiao-Chi
APPLICANT: Fend, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Richard
APPLICANT: Weber, Richard
APPLICANT: ANTEROF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING PATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 238
LENGTH: 125
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; Sequence 18, Application US/10665383
; Publication No. US20040141969A1
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Db 63 FQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGTTVT 122

Qy 123 VSS 125

Db 123 VSS 125

Search completed: April 25, 2007, 04:22:50

Job time: 47.2571 secs
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US-11-109-181-48
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Sequence 317, App
Sequence 203, App
Sequence 203, App
Sequence 240, App
Sequence 341, App
Sequence 19, Appl
Sequence 201, Appl
Sequence 288, App
Sequence 288, App
Sequence 218, App
Sequence 214, Appl
Sequence 241, Appl
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                                                                                                      April 25, 2007, 04:23:02; Search time 48 Seconds (without alignments) 533.620 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-11-109-181-200

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US-11-109-181-373

US-11-109-181-203

US-11-109-181-203

US-11-109-181-203

US-11-109-181-204

US-11-109-181-204

US-11-109-181-208

US-11-109-181-208

US-11-109-181-204

US-11-109-181-241

US-11-109-181-241

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US-11-311-939-429
US-11-109-181-21
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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Sequence 199, App	Sequence 236, App		Sequence 37, Appl	202,	Sequence 239, App	_		22,	Sequence 49, Appl	9	Sequence 14, Appl	Sequence 22, Appl	Sequence 46, Appl	Sequence 81, Appl	Sequence 28, Appl	Sequence 26, Appl	Sequence 154, App	Sequence 27, Appl	Sequence 27, Appl	
US-11-109-181-199	US-11-109-181-236	US-11-109-181-294	US-11-109-181-37	US-11-109-181-202	US-11-109-181-239	US-11-311-939-586	US-11-410-886-69	US-11-410-886-22	US-11-410-886-49	US-11-410-886-6	US-11-433-924-14	US-11-304-986-22	US-11-303-478-46	US-11-305-899-81	US-11-484-456A-28	US-11-484-456A-26	US-11-433-924-154	US-09-784-950-27	US-11-366-003-27	
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84.4	84.4	84.4	83.6	83.6	83.6	83.1	82.7	82.7	82.0	82.0	81.3	90.6	90.6	9.08	9.08	80.4	80.1	79.9	79.9	
567.5	567.5	567.5	561.5	561.5	561.5	558.5	556	556	551	551	546.5	541.5	541.5	541.5	541.5	540.5	538.5	537	537	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

ö 120 120 9 9 61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY ö Query Match 100.0%; Score 672; DB 7; Length 125; Best Local Similarity 100.0%; Pred. No. 7.9e-56; Matches 125; Conservative 0; Mismatches 0; Indels APPLICANT: Corvalina, Jose R.F.
APPLICANT: Corvalina, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Grait, Gadi
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 125 Sequence 48, Application US/11109181 Publication No. US20060293506A1 GENERAL INFORMATION: ORGANISM: homo sapiens 121 VTVSS 125 121 VTVSS 125

RESULT 2 US-11-109-181-200 ; Sequence 200, Application US/11109181

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APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng, Xiao
Yang, Xiao-Dong
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Weber, Richard
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CORGANISM: homo sapiens
US-11-109-181-372
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                                                    APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TYGIE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2005-04-18
PRIOR FILING DATE: 2005-01-07
NUMBER: OF SEQ ID NOS: 377
SOTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 200
LENGTH: 125
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO COMPANY
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
COURTER PRESED FREESEQ FOR WINDOWS Version 4.0
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Pred. No. 7.9e-56;
; Mismatches 0;
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100.0%;
Publication No. US20060293506A1
                                     APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 100.
Matches 125; Conservative
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ORGANISM: homo sapiens
US-11-109-181-237
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ORGANISM: homo sapiens
US-11-109-181-200
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LENGTH: 125
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61 AQKFQGRVTWITRDISISTAYMELSSLRSEDTAIYXCVRGFGYSYNYDYYYGMDVWGQGTT 120
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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: ADENIX: 0.51.

CURRENT APPLICATION NUMBER: US/11/109,181

CURRENT FILING DATE: 2005-04-18

PRIOR PILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FateSEQ for Windows Version 4.0

ENGTH: 125

LENGTH: 125
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Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Via, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 372, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
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Query Match
Best Local Similarity 94.4%;
Matches 118; Conservative
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ORGANISM: homo sapiens
US-11-109-181-240
      121 VTVSS 125
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen;
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
APPLICANT: Branch, Binyam
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Pred. ...
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 125
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CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 125
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Best Local Similarity 94.43
Matches 118; Conservative
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Matches 118; Conservative
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ORGANISM: homo sapiens
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ORGANISM: homo sapiens
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RESULT 7

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61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGT 119
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Sequence 201, Application US/11109181

FUDIcation No. US20060293506A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Bichard

APPLICANT: Weber, Boon

SEQ ID NO 201

LENGTH: 126

TUBER TERRESON OF SEQ ID NOS: 377

SOFTWARE: FEATSEQ for Windows Version 4.0

SEQ ID NO 201

LENGTH: 126
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                     APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT APPLICATION NUMBER: US/11/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
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89.7%; Pred. No. 2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 593.5; DB
Pred. No. 2e-48;
4; Mismatches
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89.7%;
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Best Local Similarity 89.77
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 113; Conservative
Weber, Richard
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CAGANISM: homo sapiens
US-11-109-181-19
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ORGANISM: homo sapiens
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Best Local Similarity
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APPLICANT: Belouski, Shelley Sims
APPLICANT: Green, Larry L.
TITLE OF INVENTION: URRY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
TITLE OF INVENTION: OTHER DISORDERS
FILE REPERENCE: ABGENIX.120A
CURRENT PELLING DATE: 2006-05-12
PRIOR FILING DATE: 2006-05-16
PRIOR FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYGYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTRNTS1STAYMELSSLRSEDTAVYYCARGYSSSWYRGYYYYYGMDVWGQG 120
                                                                                                                                                                                                                                                                                            61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                   Gaps
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0
                                                                         Score 638; DB 7; Length 125;
Pred. No. 1.3e-52;
3; Mismatches 4; Indels
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Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-433-924-94; Sequence 94, Application US/11433924; Publication No. US20060286112A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kellermann, Sirid-Aimee
                                                                         Query Match
Best Local Similarity 94.4%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 89.7
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-433-924-94
  ORGANISM: homo sapiens
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US-11-109-181-343
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US-11-109-181-19
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86.2%;
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Matches 110; Conservative
                                       ; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-238
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ORGANISM: Homo sapiens
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Best Local Similarity
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SEQ ID NO 238
LENGTH: 125
                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF PLE REFERENCE: ANGINE TO STATE OF THE PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR PLILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                            ; Sequence 288, Application US/11109181; Publication No. US20060293506A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: homo sapiens
US-11-109-181-288
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                  120 TVTVSS 125
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US-11-109-181-288
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APPLICANT: Rellemann, Sirid-Aimee
APPLICANT: Foord, Orit
APPLICANT: Foord, Orit
APPLICANT: Belouski, Shelley Sims
APPLICANT: Belouski, Shelley Sims
APPLICANT: Green, Larry L.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
TITLE OF INVENTION: OTHER DISORDERS
TITLE OF INVENTION: OTHER DISORDERS
TITLE OF INVENTION: OTHER DISORDERS
TITLE OF INVENTION: 2004
CURRENT APPLICATION NUMBER: US/11/433,924
CURRENT FILING DATE: 2006-05-12
PRIOR APPLICATION NUMBER: US 60/681,846
PRIOR APPLICATION NUMBER: US 60/681,846
PRIOR PRING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 419
SOFTWARE: PSESEG for Windows Version 4.0
SEQ ID NO 254
LENGTH: 122
                                                                                                                                                                                                                                                       64 FQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYYYGMDVWGQGTTVT 122
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                                                                                                                             4 LVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQK
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Score 579.5; DB 7; Length 125;
Pred. No. 4e-47;
4; Mismatches 8; Indels 1;
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(WS-11-109-181-40)
(S-11-109-181-40)
(Sequence 40, Application US/11109181)
(Publication No. US20060293506A1)
(GENERAL INFORMATION:
(APPLICANT: Corvalan, Jose R.F.)
(APPLICANT: Feng, Xiao-Chi
(APPLICANT: Feng, Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 254, Application US/11433924
Publication No. US20060286112A1
GENERAL INFORMATION:
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Yang, Xiao-Dong

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYXCARDIVVVVTATDYYYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
85.6%; Score 575.5; DB 7; Length 126;
Best Local Similarity 87.3%; Pred. No. 9.7e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezaber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REPERBENCE: ADGENIX. 051A
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ 'ID NO 40
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 25, 2007, 04:27:43 Job time: 48.1992 secs
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
, ORGANISM: homo sapiens
US-11-109-181-40
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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protein search, using sw model OM protein - Run on:

April 25, 2007, 03:54:56; Search time 94 Seconds (without alignments) 564.248 Million cell updates/sec

US-10-665-383-4 Title: Perfect score:

Sequence:

1 EIVLTQSPGTLSLSPGERAT........CQQYGSSPCSFGQGTKLEIK 108

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

2782304 Total number of hits satisfying chosen parameters:

2782304 seqs, 489333398 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_200701:\* 1: genesem1000. Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2005s:\* geneseqp2006s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2002s:\* geneseqp2004s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2007s:\*

# SUMMARIES

		de			SUPERLES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	558	100.0	108	7	ADK18625	Adk18625 Anti-huma
7	558	100.0	108	7	ADK18951	Adk18951 Anti-huma
m	558	100.0	108	7	ADK18835	Adk18835 Anti-huma
4	558	100.0	108	7	ADK18801	Adk18801 Anti-huma
'n	558	100.0	108	œ	ADL25394	Adl25394 Human mAb
9	543	97.3	109	10	AEF73695	Aef73695 Human IL-
ŗ	543	97.3	236	10	AEF73710	Aef73710 Human IL-
ω	535	95.9	108	σ	ADY26769	Ady26769 Anti-NGF-
σ	535	95.9	108	σ	ADY26816	Ady26816 Human ant
10	535	95.9	128	σ	ADZ57709	Adz57709 Germline
11	535	95.9	129	7	AAR38672	Aar38672 vk325-Jk2
12	533	95.5	108	7	ADP03986	Adp03986 Murine-ex
13	533	95.5	120	10	AEH89253	Aeh89253 Anti-VEGF
14	533	95.5	130	9	ABJ36930	Abj36930 Anti-CD40
12	533	95.5	130	10	AEG95253	Aeg95253 Human imm
16	533	95.5	140	10	AEH89279	Aeh89279 Anti-VEGF
17	533	95.5	384	4	AAM24101	Aam24101 Human EST
18	532	95.3	108	80	ADQ16703	Adq16703 Modified
19	532	95.3	108	6	ADV44439	Adv44439 pAX116 va
20	532	95.3	108	σ	AEB12911	Aeb12911 Antibody
21	532	95.3	108	σ	AEC81271	Aec81271 Human mon
22	532	95.3	108	თ	AEC81269	Aec81269 Human mon

Aec81267 Human mon Aef81808 Human ant Aef81806 Human ant Aef81804 Human ant	Adp46971 Murine li Aei65167 Anti-Ang- Adv44477 Anti-teta	Aee03759 Antibody Add40551 3E1/4G11 Aeb12948 Antibody		Aeb12910 Antibody Adv44458 Anti-teta	Antib Ig L		Aea89845 Anti-IFN Aau14462 Human nov	Human Human	Aaul4464 Human nov
9 AEC81267 10 AEF81808 10 AEF81806 10 AEF81804	8 ADP46971 10 AEI65167 9 ADV44477	10 AEE03759 7 ADD40551 9 AEB12948	800	9 AEB12910 9 ADV44458	თ თ	00	9 AEA89845 4 AAU14462	4 AAU14463 4 AAU14461	4 AAU14464
.3 108 .3 108 .3 108	.3 109 .3 109 .3 112	.3 115 .3 120	.3 215	.3 215 .3 239	.3 239 .2 108			95.0 384 95.0 384	.0 384
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23 25 26 26	27 28 29	331	333	35 36	37 38	39 40	41 42	4 4 4	45

### ALIGNMENTS

Anti-human PDGF-D antibody light chain protein sequence. ADK18625 standard; protein; 108 AA. 06-MAY-2004 (first entry) Homo sapiens. ADK18625; RESULT 1 ADK18625 

antiinflammatory; immunomodulator; cytostatic; gene therapy. WO2003057857-A2. 17-JUL-2003

(ABGE-) ABGENIX INC

06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860.

Weber R; Gazit G, Chen F, Yang X, Feng X, Corvalan JRF, Jia X, Bezabeh B;

WPI; 2003-587119/55.

growth New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 49; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

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ADK1883
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                                                                                                                                                       EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                                                                                                                                                                                                                                                                        DRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                 Length 108;
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                                                               Score 558; DB 7;
Pred. No. 4.6e-35;
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100.0%; Pred. No. 4.6e-35;
iive 0; Mismatches 0;
                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        ADK18951 standard; protein; 108 AA
                                          100.0%; Sc.
100.0%; Pre
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                                                                                                             Matches 108; Conservative
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                                                                                      Local Similarity
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                     Sequence 108 AA;
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The invention, relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; immunomodulator; cytostatic; gene therapy
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Matches 108; Conservative
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Local Similarity 100. 1es 108; Conservative

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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108

Lichenstein H;

Larochelle WJ,

Keyt B,

Gazit-Bornstein G,

Floege J,

WPI; 2004-269881/25. N-PSDB; ADL25393

(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.

16-SEP-2003; 2003WO-US029414 16-SEP-2002; 2002US-0411137P

25-MAR-2004

Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating

Disclosure; SEQ ID NO 4; 115pp; English.

nephritis.

ж, Weber

Gazit G,

Chen F,

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Autibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                   factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                  New human monoclonal antibody that binds to platelet-derived
                                antiinflammatory; immunomodulator; cytostatic; gene therapy
Anti-human PDGF-D antibody protein related sequence #27.
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100.0%; Pred. No. 4.6e-35;
ive 0; Mismatches 0;
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                                                                                            WO2003057857-A2
                                                                Homo sapiens
                                                                                                                                                                                                                                                                       Bezabeh B;
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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

(1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting menangial cell proliferation; and (4) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antihiflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclomal antibody (mAD) variable region sequence, which is used in the exemplification of the present invention.

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/label= L-CDR2
90. .98
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antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

Human mAb 6.4 light chain variable region protein SEQ ID NO:4.

17-JUN-2004 (first entry)

nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.

WO2004024098-A2

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Gaps

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0; Indels

Length 108;

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The present invention relates to interleukin-17 (IL-17) antagonistic antibodies suitable for use in the treatment of IL-17 mediated diseases and disorders. A claimed IL-17 binding molecule is capable of inhibiting the activity of 1 nM human IL-17 binding molecule is capable of inhibiting the activity of 1 nM human IL-17 and interleukin-6 production induced by the activity being measured on interleukin-6 production induced by comprises: a heavy chain variable region (DR) ABE73686-ABE7368 (Comprising complementarity determining regions CDR1, CDR2 and CDR3 ABE73686-ABE7369 from anti-human IL-17 antibody AIN457; and a light chain variable region (LH) comprising CDR1, CDR2, and CDR3, CDR2, ABE73689 from anti-human IL-17 antibody AIN457; and IL-17 binding molecule is preferably comprising a first domain having amino acid sequence homology. It preferably comprises at least one antigen binding site comprising a first domain having amino acid sequence homology to the AIN457 VL region ABE73695. Also provided are a DNA comprising a first domain having amino acid sequence homology to the AIN457 VL region ABE73695. Also provided are a DNA construct encoding the IL-17 binding molecule by culturing a transformed host cell line. The construct encoding the DNA construct, and a method of producing an IL-17 binding molecule by culturing a transformed host cell line. The creatment of an IL-17 mediated disease or disorder, especially osteoarthritis, rheumatoid arthritis, osteoporosis and other inflammatory architic is engineered to express the human IgG/kappa repertoire instead of the murine immunoglobulin repertoire, was used to generate antibodies to human IL-17. B-cells from these mice were immortalized by standard hybridoma technology and murine hybridoma cells were obtained else secreted the human IgG1/kappa antibody AIN457. The present sequence is the amino acid sequence of AIN457 VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel interleukin-17 binding molecule capable of inhibiting human IL-17 activity and IL-6 production induced by human-IL-17 in human dermal fibroblasts, useful for treating IL-mediated diseases e.g. osteoarthritis.
                                                                                                                                                                                                                                                                                                       Jeschke M, Rondeau J;
                                                                                                                                                                                                                                                                                                       Hofstetter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 10; 76pp; English.
/label= L-CDR3
                                                                                                                                       04-AUG-2005; 2005WO-EP008470.
                                                                                                                                                                                                                                 (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
                                                                                                                                                                                     05-AUG-2004; 2004GB-00017487
                                                                                                                                                                                                                                                                                                       Gram H,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2006-145760/15.
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AEF73694
                                              WO2006013107-A1.
                                                                                                                                                                                                                                                                                                                             Van Den Berg W;
                                                                                                                                                                                                                                                                                                     Di Padova FE,
                                                                                            09-FEB-2006.
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60 Length 109; .. 2 97.3%; Score 543; DB 10; 96.3%; Pred. No. 6.4e-34; iive 2; Mismatches 2; Best\_Local Similarity 96.3 Matches 104; Conservative Sequence 109 AA; Query Match

Gaps

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Indels

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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPCTFGGGTRLEIK 108

RESULT 7 AEF73710 ID AEF7:

AEF73710 standard; protein; 236 AA

AEF73710;

06-APR-2006 (first entry)

Human IL-17 antibody AIN457 light chain.

Interleukin-17 antagonist, antibody production, antibody therapy, osteoarthritis, rheumatoid arthritis, osteoporosis; inflammation; antiarhritis, antiheumatic, osteopathic; antiinflammatory; musculoskeletal disease; immune disorder; inflammation; degeneration; endocrine disease; light chain.

Homo sapiens

Location/Qualifiers 45. .56 /label= L-CDR1 Region

/label= L-CDR2 111. .119 /label= L-CDR3 94. Region Region

WO2006013107-A1

09-FEB-2006

04-AUG-2005; 2005WO-EP008470.

05-AUG-2004; 2004GB-00017487

(NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS PHARMA GMBH.

Gram H, Hofstetter H, Jeschke M, /an Den Berg W; Di Padova FE,

Rondeau J;

Novel interleukin-17 binding molecule capable of inhibiting human IL-17 activity and IL-6 production induced by human-IL-17 in human dermal fibroblasts, useful for treating IL-mediated diseases e.g. WPI; 2006-145760/15

Example 3; Page 43-44; 76pp; English.

osteoarthritis.

The present invention relates to interleukin-17 (IL-17) antagonistic antibodies suitable for use in the treatment of IL-17 mediated diseases and disorders. A claimed IL-17 binding molecule is capable of inhibiting the activity of 1 mM human IL-17 binding molecule is capable of inhibiting the activity of 1 mM human IL-17 a concentration of less than 5 mM by 50%, the activity being measured on interleukin-6 production induced by human IL-17 in human dermal fibroblasts. The IL-17 binding molecule comprises: a heavy chain variable region (VH) comprising complementarity determining regions CDR1, CDR2 and CDR3 ABF73686-ABF7368 or CDR1-x, CDR2 x and CDR3-x ABF73698 from anti-human IL-17 antibody AIN457; and a light chain variable region (LH) comprising CDR1, CDR2 and CDR3 ABF73699-ABF73699 from AIN457. The IL-17 binding molecule is preferably comprising after comprising after the first domain having anno acid sequence homology to the AIN457 VL region ABF73695. Also provided are a DNA construct encoding the IL-17 binding molecule by culturing a transformed host cell line. The LI-17 binding molecule is used to manufacture; especially crecarchritis, rheumatoid arthriting a transformed host cell line. The treatment of an IL-17 mediated disease or disorder, especially arthritides. In an example from the invention, transgenic mouse 27340, which is engineered to express the human IGG/Asppa repertoire antibodies to the murine immunorlobulin repertoire, was used to generate antibodies to the murine immunoglobulin repertoire, was used to generate antibodies to human IL-17. B-cells from these mice were immortalized by standard hybridoma technology and murine hybridoma cells were obtained which secreted the human IgG1/kappa antibody AIN457. The present sequence is ;

Gaps

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Length 108;

Score 535; DB 9; Length 10c Pred. No. 2.6e-33; Pred. ----hes 3; Indels

95.9%;

1; Mismatches

Matches 104; Conservative

Similarity

Query Match Best Local

Sequence 108 AA;

9 9

1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYVASSRATGIP 1 EIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP

DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108

61

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This is the amino acid

comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain variable region.

vector comprising the above polynucleotide; and a host cell

expression

88888888888

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human anti-nerve growth factor (NGF) neutralizing antibodies useful manufacturing a medicament for treating painful disorders (e.g. acute 1) or conditions associated with increased expression or sensitivity
                                                                                                    RIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPKLLIYGASSRATGIP 81
                                                                                   9
                                                                                 BIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                              Gaps
                                                                                                                                                                                                                                                                               analgesic; gene therapy; antibody engineering; pharmaceutical; pain; neurological disease; NGF; nerve growth factor; light chain variable region.
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                                                              ö
                                                                                                                           DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                      DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCTFGQGTRLEIK 129
                                          Length 236;
                                                                                                                                                                                                                                                             Anti-NGF-antibody light chain variable region SEQ ID NO 84.
                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang
                                       Score 543; DB 10;
Pred. No. 1.3e-33;
2; Mismatches 2;
the amino acid sequence of AIN457 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inoue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 33; SEQ ID NO 84; 190pp; English.
                                                                                                                                                                                                 ADY26769 standard; protein; 108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang
                                         97.3%;
                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004; 2004WO-US022876.
                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2003; 2003US-0487431P
                                                                                                                                                                                                                                         (first entry)
                                                             104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild KD, Treanor JJS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human anti-nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-202606/21.
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                     Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                              WO2005019266-A2
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                        19-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                    03-MAR-2005
                                                                                                                                             82
                                                                                                                                                                                                                     ADY26769;
                                        Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pain)
                                                                                                                                                                                      RESULT
SXS
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The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described area methods of treating a condition a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising my of the 59 amino acid sequences comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a pharmaceutical cannot of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical New human anti-nerve growth factor (NGF) neutralizing antibodies useful for manufacturing a medicament for treating painful disorders (e.g. acute pain) or conditions associated with increased expression or sensitivity analgesic; gene therapy; antibody engineering; pharmaceutical; pain; neurological disease; NGF; nerve growth factor; light chain. DRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPYTFGQGTKLEIK 108 Martin Zhang TJ, Human anti-NGF-antibody light chain SEQ ID NO 131. Inoue H, Claim 33; SEQ ID NO 131; 190pp; English. Æ ï ADY26816 standard; protein; 108 Huang 15-JUL-2004; 2004WO-US022876 15-JUL-2003; 2003US-0487431P 19-MAY-2005 (first entry) WPI; 2005-202606/21. (AMGE-) AMGEN INC. WO2005019266-A2 Homo sapiens 03-MAR-2005, ADY26816; Wild KD, NGF. 셤

The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF in a patient; methods for detecting any of the 59 amino acid sequences comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF, a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an isolated cell line that encodes the above antibody or binding agent; an

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antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain.
of the monoclonal antibody or the fragment, where the monoclonal
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Sequence 108 AA;

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EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                              EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                            Gaps
                                              ;
0
                                                                                                                                                                                                   DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGQGTKLEIK.108
                                                                                                                                                                          61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
95.9%; Score 535; DB 9; Length 108; 96.3%; Pred. No. 2.6e-33; Indels iive 1; Mismatches 3; Indels
                        Best Local Similarity 96.3
Matches 104; Conservative
      Query Match
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RESULT 10

ADZ57709 standard; protein; 128 AA ADZ57709;

30-JUN-2005 (first entry)

Germline antibody A27Vk3,Jk2 light chain protein.

antibody engineering; cytostatic; vulnerary; vasotropic; cardiant; monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer; gastrointestinal ulcer; ischemia; transplant rejection; myocardial infarction; reperfusion injury; restenosis; angioplasty; vascular disease; cancer; retinopathy; endometriosis; arthritis; Alzheimers disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis; antibody. 

Homo sapiens

09-FEB-2005

04-AUG-2004; 2004GB-00017384

04-AUG-2003; 2003US-0492432P

(PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.

Green LL; Coleman K, Bedian V, Borzillo G, Michaud NR, Kajiji S, Jia X;

WPI; 2005-145169/16.

Human monoclonal antibody or antigen-binding portion that specifically binds to c-Met, useful for treating cancer by inhibiting c-Met or for promoting tissue regeneration and wound healing by activating c-Met.

Example 2; SEQ ID NO 18; 128pp; English.

The invention relates to a human monoclonal antibody (I) or its antigenbinding portion that specifically binds to c-Met, comprises a heavy chain having a fully defined sequence (SI) of 13.3.2 heavy chain, where X2 is

Region

lysine and X4 is threonine, and a light chain having a fully defined sequence (\$2) of 13.3.2 light chain, where X8 is threonine, where both chains are without a signal sequence. All the sequences are fully defined in the specification. (I) is useful for the manufacture of a medicament for treating a hyperproliferative disorder in a subject, where the manufacture of a medicament for promoting wound healing or tissue regeneration in a subject, where the antibody, antigen-binding portion or regeneration activates c-Met. (I) which has a c-Met agonist activity is useful in tissue regeneration or wound healing (skin ulcers or gastric ulcers), or treating ischemia associated with kidney transplant regeneration for treating ischemia associated with kidney transplant curgery, for treating myocardial infarction, cardiac rejection, for attenuating toxicity associated with cardiac ischemia due to reperfusion injury, restenosis after angloplasty or vascular diseases. (I) which has a c-Met antagonist activity is useful contexting and arthritis, for inhibiting plaque for treating cancers of brain, lung, squamous cell, bladder, neck, liver, prostate, etc., proliferative vitrecentinopathy, proliferative diabetic responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas. (I) is useful for detecting c-Met in a biological sample in vitro or in vivo, thus useful for dangenesting c-Met in a biological sample in vitro or in vivo, thus useful for dangenesting c-Met in a biological sample in vitro or in vivo, thus useful for datecting c-Met in a biological sample in vitro or in corresponds to the amino acid sequence for a germline antibody light BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80 Gaps . 0 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 DRFSGSGSGTDFTLTISRLEPEDFAVYXCQQYGSSPYTFGQGTKLEIK 128 95.9%; Score 535; DB 9; Length 128; 96.3%; Pred. No. 3e-33; 3; Indels 1; Mismatches chain used in the invention. Matches 104; Conservative Query Match Best Local Similarity Sequence 128 AA; 81 ઠે 점 ઠે d

AAR38672 standard; protein; 129 AA (first entry) (revised) 25-MAR-2003 01-NOV-1993 AAR38672; RESULT 11 AAR38672

vk325-Jk2.

Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; note= "Met encoded by ATC (sic)" /note= "Pro encoded by GCA (sic)" 21. .129 /label= mat\_protein 1. .20 /label= sig\_peptide ocation/Qualifiers l. .116 /label= vk325 44. .55 /label= CDR1 71. .77 epitope; immune deficiency Misc-difference 35 Misc-difference Homo sapiens Protein Peptide Key Region Region THE HELL LEADY SON TO SEE THE SEE THE

Region

Region

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antibody production, monoclonal antibody;
vascular endothelial growth factor receptor-1; VEGFR-1;
light chain variable region, tumor; cytostatic; neoplasm;
angiogenesis disorder; antiangiogenic; cardiovascular disease;
atherosclerosis; antiarthritic; matirheumatic; immune disorder;
rheumation; musculoskeletal disease; neovascular glaucoma; retinopathy;
macular degeneration; ophthalmological; ocular disease; psoriasis;
antipsoriatic; dermatological disease; graft rejection;
immunosuppressive; insulin-dependent diabetes mellitus; antidiabetic;
endocrine disease; gastrointestinal disease; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined anino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, osesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VL (light chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
                                                                                                                                                                                                                                                                                                                                                                    New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-VEGFR-1 antibody light chain variable region SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 533; DB 7;
Pred. No. 3.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 156; 89pp; English.
                                                                                                                                                                                                                                                                                 Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEH89253 standard; protein; 120 AA
                                                                                                                                                     02-DEC-2002; 2002WO-US038550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.5%;
                                                                                                                                                                                               03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                    Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain
                                                                                                                                                                                                                                         (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                            WPI; 2003-523295/49.
                                                                                                                                                                                                                                                                                 Foltz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108 AA;
                                                                WO2003048328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-2006
                                                                                                          12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103;
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                                                                                                                                                                                                                                                                                    Gudas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                名
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other F105 Vk sequences given elsewhere in the specification) was compared with germline gene Humvk325 (AAQ42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.9%; Score 535; DB 2; Length 129; 96.3%; Pred. No. 3e-33; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haseltine WA;
                                        note= "Leu encoded by GTG (sic)"
                                                                                                                              (sic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                              'note= "Gly encoded by GAT
                                                                                                                                                                         'note= "Ser encoded by AAC
                                                                                                                                                                                                                   'note= "Pro encoded by GTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 74-75; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Posner MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP03986 standard; protein; 108 AA.
                                                              110. .117
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                            92WO-US010928
                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00804652
/label= CDR2
                                                                                                                                                                                                                                     117. .129
/label= Jk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marasco WA, Sodroski JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-214174/26.
N-PSDB; AAQ42706.
                                                                                                                                                  Misc-difference 114
                      Misc-difference
                                                                                                        Misc-difference
                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 129 AA;
                                                                                                                                                                                                                                                                                                        WO9312232-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection
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RESULT 12

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ADP03986
IID ADP0
XX ADP0
XX ADP0
XX XX ADP0
XX XX XX XX XX XX XX XX ADP0
KW COTO
KW COTO
KW COTO
KW GETV

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Gaps

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Length 108; 3; Indels 9

α

Sequence 120 AA; Wu Y, 

myasthenia gravis, muscular-gen.; neuroprotective; Crohns disease, antiinflammatory; gastrointestinal-gen.; nephritis; nephrotropic; gentrointestinal-gen.; nephritis; nephrotropic; gentrourinary disease; primary biliary cirrhosis; hepatotropic; panoreatitis, allergy; antiallergic, contact dermatitis; dermatological; delayed hypersensitivity; inflammatory bowel disease; septic shock; antibacterial; infection; osteopothosis; osteopathic; degeneration; endocrine disease; musculoskeletal disease; osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease; cognitive disorder; noncropic; hereditary hemorrhagic telangisctssia; vasotropic; restenosis; fungal infection; fungicide; parasitic infection; antiparasitic; viral infection; cytomegalovirus infection; virucide. vascular endothelial growth factor receptor-1 for treating cancers and angiogenic-related disorders, e.g. atherosclerosis. New isolated human monoclonal antibody that binds specifically to sclerosis; neuroprotective; neurological disease; Claim 6; SEQ ID NO 15; 82pp; English. 18-NOV-2004; 2004US-0628815P. Bohlen P; 18-NOV-2005; 2005WO-US041904 (IMCL-) IMCLONE SYSTEMS INC WPI; 2006-373517/38. Hicklin DJ, N-PSDB; AEH89260. WO2006055809-A2 Homo sapiens. 26-MAY-2006.

Sequence 130 AA; Mikayama T, The invention relates to an isolated human monoclonal antibody or fragment that binds specifically to vascular endothelial growth factor creceptor—1 (VEGRE-1) and comprises a light chain complementarity determining region—2 (CDR2) of 7 amino acids (SEQ DNO: 2; see AEH89240) and a light chain CDR3 of 9 amino acids (SEQ DNO: 3; see AEH89241). Also cincluded are: an isolated polymucleotide comprising a nucleotide sequence encoding an antibody or its fragment; an isolated polymucleotide sequence encoding an antibody or its fragment that specifically binds to VEGRE-1; an expression vector comprising the oplymucleotide sequence encoding an antibody or its fragment that specifically binds to VEGRE-1; an expression vector comprising the oplymucleotide sequence linked to an expression vector comprising the expression vector comprising the expression vector is method of producing an an antibody or its fragment; a method of modulating activity of VEGRE-1 in a mammal; a method of inhibiting angiogenesis in a mammal; and a method of reducing tumor growth in a mammal; and a method of angiogenesis and reduce tumor growth in a mammal. The antibody is used to inhibit angiogenic-related disorders (e.g. atherosclerosis, rheumatoid arthritis, angiogenic-related disorders (e.g. atherosclerosis, rheumatoid arthritis, psoriasis, retinopathy of prematurity (retrolental fibroplastic), corneal constants, acute panoreatitis, allogeneration, hemangiomas, angiofibromas, graft rejection, insulin-dependent diabetes mellitus, multiple sclerosis, mysthemia gravis, crothard degeneration, hemangiomas, angiofibromas, graft rejection, insulin-dependent diabetes mellitus, multiple sclerosis, mysthemia gravis, contact dermaturity (retrolental fibroplastic), corneal contact dermaticis and delayed hypersensistivity creating and elayed hypersensistivity contact dermaticis and delayed hypersensistivity. reactions, inflammatory bowel disease, septic shock, osteoporosis, osteoarthritis, cognition defects induced by neuronal inflammation, Osler-Weber syndrome (hereditary hemorrhagic telangiectasia), restenosis, and fungal, parasitic and viral infections, including cytomegaloviral infections). The present sequence represents anti-VEGFR-1 antibody light chain variable region SEQ ID NO:15. Score 533; DB 10; Length 120; Pred. No. 4e-33; 2; Mismatches 3; Indels 95.5%; Scor 95.4%; Pred

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Gaps

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Conservative

Best Local Similarity Matches 103; Conservat

Query Match

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The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LPS (lippolysaccharide) and IFNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosupperssants, and as remedies for autoimmune diseases, allergy or coaquilation factor VIII inhibitors syndrome. This sequence represents a protein relating to the anti-CD40 monoclonal antibody of the invention
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9
                      1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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                                                                                                                                                                                                                                                                                                                                              Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LP5; lipopolyaaccharide; IFWgamma; interferon gamma; dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line; immunoactivator; anti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD4 or functional fragment, is useful in the treatment of e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                        61 DRFSGSGSGTDFTLTISRLEPEDFAVYXCQQYGSSPLTFGQGTRLEIK 108
                                                                   61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.5%; Score 533; DB 6; Length 130; Best Local Similarity 95.4%; Pred. No. 4.3e-33; Matches 103; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                            Anti-CD40 monoclonal antibody related protein SEQ ID No 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Force WR,
                                                                                                                                                                                                    ABJ36930 standard; protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 51; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-2002; 2002WO-JP004292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2001; 2001WO-US013672.
11-MAY-2001; 2001JP-00142482.
05-OCT-2001; 2001JP-00310535.
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                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-120463/11.
N-PSDB; ABT31872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200288186-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                          01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2002
                                                                                                                                                                                                                                      ABJ36930;
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RESULT 15 용 ઠે

AEG95253 standard; protein; 130 AA.

01-JUN-2006 (first entry) AEG95253;

Human immunoglobulin G4 (IgG4) antibody related protein SEQ ID NO 8.

immunosuppressive; antiinflammatory; gastrointestinal-gen.; antiulcer; dermatological; hemostatic; neuroprotective; antipsoriatic; antitheumatic; cytostatic; antiarteriosclerotic; nephrotropic; immunostimulator; immunoglobulin; IgG4; transplant rejection; immune disorder; systemic lupus erythematosus; dermatological disease; metabolic disorder; musculoskeletal disease; idiopathic thrombocytopenic purpura; genetic disorder; hematological disease; neurological disease; multiple sclerosis; psoriasis; dermatological disease; rheumatism; inflammation; cancer; neoplasm; arteriosclerosis; cardiovascular disease; nephritis; genitourinary disease; Alzheimers disease; degeneration; amyloidosis.

Homo sapiens.

WO2006033386-A1.

30-MAR-2006.

22-SEP-2005; 2005WO-JP017463.

22-SEP-2004; 2004JP-00275908

(KIRI ) KIRIN BEER KK.

Takahashi N, Yoshida H;

WPI; 2006-316320/33. N-PSDB; AEG95252.

Novel anti-CD40 antibody having heavy chain constant region of human immunoglobulin G4 including substitution of arginine at specific position by lysine, threonine, methonine or leucine, useful in treating autoimmune disease and cancer.

Example 1; SEQ ID NO 8; 47pp; Japanese

The invention relates to an antibody comprising heavy chain constant region of human immunoglobulin G4 (1gG4). The antibody being anti-CD40 antibody is useful as therapetric agent of transplant rejection, autoimmune disease, cancer, arteriosclerosis, nephritis, Alzheimer's disease or amyloidosis. The antibody is useful for treating transplant rejection, autoimmune disease (e.g. inflammatory bowel disease, Crohn's cisease and ulcerative colitis), systemic lupus erythematosus (SLS), idiopathic thrombocytopenic purpura (ITP) multiple sclerosis, psoriasis, remembrism, cancer (e.g. lung cancer, colon cancer, bladder cancer, breast cancer, liver cancer, prostatic cancer, bladder cancer, breast cancer, bracker cancer, inver cancer, prostatic cancer, bladder cancer, broater cancer, prostatisms suppressed aggregation formation, and is highly stable mutant of 1gG4 antibody. The antibody exhibits decreased aggregate formation in low PH, and maintains binding controlled antibody dependent cell-mediated cytotoxicity and/or controlled antibody dependent cell-mediated cytotoxicity and/or controlled antibody dependent cell-mediated cytotoxicity and/or controlled antibody dependent cell-mediated cytotoxicity such in mumnoglobulin G4 (1gG4) antibody related protein. Note: The complement dependent cytotoxicity. The present sequence represents a chuman immunoglobulin G4 (1gG4) antibody related protein. Note: The sequence date for this pacent was obtained in electronic format directly from WIPO at ftp.wipo.int/published\_pct\_sequences. 

Sequence 130 AA;

Gaps .; Length 130; Indels 3; DB 10; Score 533; DB 10; Pred. No. 4.3e-33; 2; Mismatches 95.5**%**; 95.4**%**; Best Local Similarity 95.4 Matches 103; Conservative Query Match

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80

1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60 21 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 셤 ð

8

Search completed: April 25, 2007, 04:05:22 Job time: 94.661 secs

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 04:05:37 ; Search time 8 Seconds (without alignments) 1261.509 Million cell updates/sec

US-10-665-383-4 Perfect score:

1 EIVLTQSPGTLSLSPGERAT.......CQQYGSSPCSFGQGTKLEIK 108 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	ip
1	535	95.9	108	. 7	C30608	Ig kappa chain V-
7	535	95.9	109	7	H30601	Iq kappa chain V-
е	534	95.7	109	7	F30601	kappa
4	533	95.5	109	7	B30601	
ស	531	Š.	109	0	PH0963	kappa
9	531	95.2	109	7	D30601	Ig kappa chain V-
7	530	95.0	109	7	C30601	kappa
8	530	95.0	129	7	846369	light
0	530	95.0	134	7	S38643	kapp
10	529	94.8	109	0	G30601	kapp
11	529	94.8	129	~	849532	anti-Sm antibody 1
12	528	94.6	129	Н	КЗНОНА	kapp
13	527	94.4	128	0	S20636	Kapp
14	526	94.3	129	Н	КЗНОНІ	capp
15	524	93.9	109	Н	K3HUTI	kappa chain
16	524	93.9	109	7	F30607	kappa
17	523.5	93.8	114	7	S46375	kappa chain
18	521	93.4	109	Н	K3HUSI	kappa chain
19	520	93.2	109	ď	A30608	kappa chain
20	515	92.3	109	0	G30607	kappa chain
21	514	92.1	107	0	PH0965	Ig kappa chain V
22	514	92.1	108	7	B30608	cappa chain
23	513	91.9	124	N	S20633	cappa
24	511	91.6	121	7	S40327	cappa
25	508	91.0	109	Н	K3HUWL	cappa
26	507	90.9	110	7	S20635	Ig kappa chain V
27	504.5	90.4	108	0	E30609	Ig kappa chain V-1
	۳.	90.5	110	~	E30607	Ig kappa chain V-1
	0	90.1	108	Н	K3HUB6	cappa

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F4	H4	2	82	A3	S4	S4	표	B	S4	Ą	B2	A2	5	83	ប
~	7	Н	7	7	7	C3	~	7	~	N	N	N	~	~	N
109	108	109	130	129	110	109	104	215	129	96	116	215	118	108	116
90.0	99.9	9.6	9.68	39.4	39.2	38.7	37.5	37.5	37.2	86.9	96.9	36.7	35.8	35.5	35.1
502	501.5	200	200	499	497.5	495	488.5	488	486.5	485	485	484	479	477	475
											41				

### ALIGNMENTS

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S	C
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chain V-III region (Pie) - human (fragment)

C;Species: Homo sapiens (man) C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004

Rigoni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solos, T. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantil A;Reference number: A30601; MUTD:89215279; PMID:2496160

A,Accession: C30608 A,Status: preliminary A,Molecule type: protein A,Residues: 1-108 <GON>

A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Kcywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology < IMM>

Gaps ö Length 108; 3; Indels Score 535; DB 2; Pred. No. 3.8e-38; 1; Mismatches 3; 95.9%; Matches 104; Conservative Query Match Best Local Similarity

· 0

1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60 ò 셤

61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 ઠે

DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKLEIK 108 <u>а</u>

"Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000
C;Accession: H30601; B30601
C;Accession: H30601; B30601
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantil A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GOM1>
A;Residues: 1-109 <GOM1>
A;Cross-references: UNIPARC:UP1000011B930

A;Accession: E30601 A;Status: preliminary

A; Molecule type: protein A; Residues: 1-109 <GON2>

A; Cross-references: UNIPARC: UPI000011B930

95.9%;
Best Local Similarity 96.3%;
Matches 104; Conservative

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61

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: D30601
J; McManol. 142, 3158-3163, 1989
J; Immunol. 142, 3158-3163, 1989
A;Reference number: A30601; MUD:89215279; PMID:2496160
A;Reference number: A30601
A;Reterence number: A30601
A;Reterence number: A30601
A;Residues: Drotein
A;Residues: 1-109 <GON>
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE9
1 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: PHO963
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PHO952; MUID:92202880; PMID:1552291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q9UL78; UNIPARC:UP10000176A29
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
                                                                                                      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.2%; Score 531; DB 2; L 95.4%; Pred. No. 8.2e-38; tive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
95.2%; Score 531; DB 2;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;90-97/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;24-34/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: nucleic acid sequence not shown
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: F30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc J. Immunol: 142, 3158, 1389
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
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R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
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C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: B30601
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Pred. No. 4.6e-38;
4; Mismatches 3; Indels
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL/8; UNIPARC:UPI0000176AB7
A;Cross-references: UNIPROT:Q9UL/8; UNIPARC:UPI0000176AB7
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                   Length 109
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C;Superfamily: immunoglobulin, V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
         C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                  3; Indels
                                                                                                                                Score 535; DB 2;
Pred. No. 3.8e-38;
1; Mismatches 3;
                                       C; Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
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Query Match 95.7%; Best Local Similarity 93.5%; Matches 101; Conservative

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A; Molecule type: protein A; Residues: 1-109 <GON>

A;Status: preliminary A; Accession: F30601

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Matches 103; Conservative

Best Local Similarity

Query Match

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9 9 us-10-665-383-4.rpr

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A;Cross-references: UNIPARC:UP10001165A2; EMBL:Z27170; NID:g415955; PIDN:CAA81694.1; PIC;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rigoni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo J. Immunol. 142, 3158-3163, 1989
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A; Reference number: A30601; MUID:89215279; PMID:2496160
                                        R;Bensimon, C.; Chastagner, P.; Zouali, M. submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38643
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R;Mahmoudi, M.; Edwards, U.; Cairns, E.; Bell, D.
Rbunitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: 848797
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        06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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C.Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 530; DB 2;
Pred. No. 1.2e-37;
1; Mismatches 4;
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Pred. No. 1.2e-37;
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Matches 103; Conservative
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Best Local Similarity
                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <BEN>
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                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: 360601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantians.
A;Reference number: A30601; MUID:89215279; PMID:2496160
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A,Reference number: S46369; MUID:94313975; PMID:8039491
A,Accession: S46369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46569
R;Bensimon, C:; Chastagner, P:; Zouali, M.
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  DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                               DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIK 108
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Pred. No. 1.2e-37;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AEB
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: mRNA
A.Residues: 1-129 «BEN»
A.Cross-references: UNIPARC:UPIO000176CA5; EMBL:Z27170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-111/Domain: immunoglobulin homology <IPW+>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 530; DB 2;
Pred. No. 9.9e-38;
                                                                                                                                                                    C30601
Ig kappa chain V-III region (Pay) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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838643
19 kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
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Best Local Similarity 95.4<sup>a</sup>
Matches 103; Conservative
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Matches 102; Conservative
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <LEE>
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A; Residues: 1-129 <KIP>
A; Accession: S20636
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K3HUTI
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A;Map position: 2pl2-2pl1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
                         A;Cross-references: UNIPARC:UP10001166FC; EMBL:Z46345; NID:g560843; PIDN:CAA86464.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-111/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: autoantibody; chronic Tymphocytic Teukemia; heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG> F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT> F;21-117/Region: V segment F;21-117/Region: V segment F;21-117/Region: V segment
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C,Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V-III region (Hah) - human C;Species: Homo sapiens (man) C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004 C;Accession: PL0022
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Pred. No. 1.7e-37;
3; Mismatches 3; Indels
                                                                                                                                    94.8%; Score 529; DB 2; Length 129; 95.4%; Pred. No. 1.4e-37; ive 1; Mismatches 4; Indels
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Best Local Similarity 94.4%;
Matches 102; Conservative
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                                                                                                                                                                                                 Matches 103; Conservative
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A; Residues: 1-129 < KIP>
                                                                                                                                                                    Best Local Similarity
A;Residues: 1-129 <MAH>
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                                                                                                                                             Query Match
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S20636
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A,Cross-references: UNIPARC:UPI00001163DC; EMBL:Z11894; NID:g33200; PIDN:CAA77948.1; PID:
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 167, 4810-852, 1988
A,FITLE: Autoantibody-associated kappa light chain variable region gene expressed in chrc
A,Reference number: PL0021; MUID:88171307; PMID:3127527
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C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed ir
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A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp complex: An immunoglobulin heterotetramer subunit subunits associate into land disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into land c;Superfamily: immunoglobulin V region; immunoglobulin homology with the subunits associate into land C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin F;1-120/Domain: signal sequence #status predicted <SIG> F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT> F;21-117/Region: V segment
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C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor V-III region (Hic) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
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                                                                                                                                                                                                           Length 128;
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                                                                                                                                                                                                                                                                                            4: Indels
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                                                                                                                                                                                                       / Match 94.4%; Score 527; DB 2; Local Similarity 94.4%; Pred. No. 2.1e-37; nes 102; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-55/Region: complementarity-determining 1
171-77/Region: complementarity-determining 2
110-117/Region: complementarity-determining 2
1110-1217/Region: J segment (JKI)
143-109/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4
Matches 102; Conservative
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C; Accession: A01895
R; Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A; Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sut A; Accession: A01895
A; Molecule type: protein
A; Residues: 1-109 <SUT>
A; Cross-references: UNIPROT: P01622; UNIPARC: UP1000012E15D
A; Molecule type: protein
A; Residues: 1-109 <SUT>
A; Cross-references: UNIPROT: P01622; UNIPARC: UP1000012E15D
A; Note: the sequence of the C region, which has the Inv (3) marker, is also given C; Comment: This is a Bence Jones protein.
C; Comment: This is a Bence Jones protein.
C; Comment: GDB: 136266
A; Map position: 2p12-2p11
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
F; 16-91/Domain: immunoglobulin homology <IMM>F; 23-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 3.2e-37;
Matches 100; Conservative 5; Mismatches 3; Indels
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 g ò

Search completed: April 25, 2007, 04:06:40 Job time : 8.23729 secs

1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60

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Gaps ö

GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

April 25, 2007, 03:58:23 ; Search time 74 Seconds (without alignments) 1574.822 Million cell updates/sec Run on:

US-10-665;383-4 558 1 BIVLTQSPGTLSLSPGERAT......CQQYGSSPCSFGQGTKLEIK 108 Title: Perfect score:

Sequence:

Scoring table:

3281787 seqs, 1072124677 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

3281787 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_8.4:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien
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	Description	P18135	ဖ	P01622	P01620	09ul78	P01623	06pil8		P01619	P04206	Q6pjf2	Qegmv9										Qegmwo ]	P01625 ]		P06314 ]	-	P01600 ]	Q6pih7	Q9u177	P06313 ]	05n170 1
SUMMARIES		HUMAN	HUMAN	HUMAN	HUMAN	Q9UL78_HUMAN	HUMAN	OGPILS HUMAN	O9UL86_HUMAN	HUMAN	HUMAN	Q6PJF2 HUMAN	HUMAN	Q6P5S8_HUMAN	HUMAN	HUMAN	HUMAN	DE69I9 HUMAN	HUMAN	29UL83 HUMAN	29UL85_HUMAN	HUMAN	OGGMWO_HUMAN	HUMAN	HUMAN	KV4C HUMAN	HUMAN	HUMAN	26PIH7 HUMAN	29UL77 HUMAN	HUMAN	_HUMAIN
S	a a	KV3L I	KV3M_I	KV3D HUMAN	KV3B HUMAN	09UL78	KV3E HUMAN	Q6PIL	O9UL8	KV3A_HUMAN	KV3G_1	Q6PJF;	O6GMV	QEPSS	KV3C HUMAN	KV3K I	KV3F_F	056919	KV3H HUMAN	O9ULB	09UL8	KV31_HUMAN	OEGMW(	KV4A_HUMAN	KV3J_HUMAN	KV4C F	O9UL79	KV1H HUMAN	Q6PIH7	09UL77	KV4B F	OBUL70
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	* Query Match Length	129	129	109	109	109	109	236	109	108	109	235	235	236	100	128	109	234	129	108	109	115	235	114	116	134	108	108	236	108	133	108
•	A Query Match	94.6	94.3	93.9	93.4	95.8	91.0	8.06	90.3	90.1	9.68	88.4	88.0	86.3	83.5	83.4	79.9	79.8	78.7	78.0	76.3	75.4	75.3	74.5	74.2	71.6	71.4	71.2	7.07	70.0	69.4	69.3
	Score	528	526	524	521	518	508	506.5	504	503	200	493	491	481.5	466	465.5	446	445.5	439	435.5	426	420.5	420	415.5	414	399.5	398.5	397.5	394.5	390.5	387	386.5
	Result No.	1	7	e	4	S	ø	7	8	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 25	56	27	28	29	30	31

Q6gmx8 homo sapien Q8k1f1 mus musculu Q811c3 mus musculu Q811c3 mus musculu P01605 homo sapien Q723y4 homo sapien Q65zC8 homo sapien P01598 homo sapien Q72473 homo sapien Q72473 homo sapien Q65zC9 homo sapien
QGGWXB HUMAN QBKLF1_MOUSE QBJ1C3_MOUSE KV1M HUMAN QG5XC8 HUMAN Q7Z3Y4_HUMAN Q96SAZ08 HUMAN Q96SAZ08 HUMAN KV1F HUMAN KV1F HUMAN Q7Z473 HUMAN Q7Z473 HUMAN Q6ZC9_HUMAN Q6SZC9_HUMAN
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698.3 688.7 688.5 688.5 688.5 67.7 67.7
386.5 381.5 382.5 382.5 382.5 382.5 381.5 381.5 377.5 377.5
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### ALIGNMENTS

	RESULT 1  KV31 HUMAN  RV 1 HUMAN  AC P1813  DJ 01-NO  DJ 10-NO  DJ 30-MAD  CC C CALL  RR KIPPS  RR KIPPS  RR KIPPS  RR KIPPS  RR CC COPY  CC C C COPY  CC C C COPY  CC C C C C C C C C C C C C C C C C C
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KV3D HUMAN
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                                                                                                                                                                                                         1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUCLEOTIDE SEQUENCE.
MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
J. Exp. Med. 167:840-852(1988).
autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-III region HIC.
/FTId=PRO 0000015180.
Framework-1.
                                                                                                          Score 528; DB 1; Length 129;
Pred. No. 2.1e-47;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1.
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JK1 segment.
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HSSP; P01625; IEEQ.

SNR; P18136; 21-129.

Ensembl; ENGG0000169769; Homo sapiens.
LinkHub; P18136; --

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0005855; P:immune response; NAS.

InterPro; IPR007110; Ig-like.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR01406; Ig-V-set.
INTERPRO; ISR00409; IG: I.

SNART; SM00409; IG: I.

FROSITE; PS50835; IG LIKE; I.

FROSITE; PS50835; IG LIKE; I.

InterPro; IRR00406; IGV: II.

INTERPROSITE; PS50835; IG LIKE; I.

INTERPROSITE; PS50835; IG LIKE; II.

INTERPROSITE; PS50835; IG LIKE; II.
119 129 JKI segment.
43 109 By similarity.
129 129 129 129 129 AA; 14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990, integrated into UniProtKB/Swiss-Prot. 01-NOV-1990, sequence version 1. 30-MAY-2006, entry version 43. Ig kappa chain V-III region HIC precursor. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA
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                                                                                                             Query Match
Best Local Similarity 94.4%;
Matches 102; Conservative
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P18136:
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                                                                                                                  Query Match
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R RSSP, P01625; LIVE.

R GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001359; Ig-wet.

R InterPro; IPR001359; Ig-wet.

R InterPro; IPR001359; Ig-wet.

R InterPro; IPR001359; Ig-wet.

R Ffam; PF07686; V-Set; 1.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IG; 1.

R PROSITE; PS50835; IG LIKE; 1.

R PROSITE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=72188439; PubMed=5027703;
MEDLINE=72188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., arnikol H.U., Watanabe S., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."; ara.1849-208(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                Gaps
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                93.9%; Score 524; DB 1; Length 109; 92.6%; Pred. No. 4.6e-47; Live 5; Mismatches 3; Indels
                                                                                                                    Length 129;
                                                                                                                 Match

Jocal Similarity 94.4%; Pred. No. 3.5e-47;

Mismatches 4; Indels

Matches 4; Indels
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43 109 By similarity.
129 129
129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986, integrated into UniProtKB/Swiss-Prot.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA.
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Matches 100; Conservative
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us-10-665-383-4.rup

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antigen.
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 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
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                                                                                                                                                                                                                                                                                                                                                                                                          Andrews D.W., Capra J.D., "Amino acid sequence of the variable regions of light chains from tidiotypically cross-reactive human IgM anti-gamma-globulins of the
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                  DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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/FTId=PRO_0000059763.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01892; K3HUSI.
HSSP; P01625; 1LVE.
SNR; P01626; 1LVE.
SNR; P01626; 1-109.
GO; GO: CO00576; C: extracellular region; NAS.
GO; GO: O003823; F: antigen binding; NAS.
GO; GO: O005765; P: immune response; NAS.
InterPro; IPR00310; Ig-lub.
InterPro; IPR013106; Ig-lub.
InterPro; IPR013106; Ig-V=set.
INTERPROSITE; PSS00835; IG-LIKE; I.
IPR05ITE; PSS00835; IG-LIKE; I.
IPR05ITE; PSS00835; IG-LIKE; I.
IPR05ITE; PSS00835; IG-LIKE; I.
                                                                                                                                                                                          21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 42. 19 kappa chain V-III region SIE. Homo sapiens (Human).
                                                                                                                                                           109 AA.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=82046598; PubMed=6794615;
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nes 100; Conservative
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                                                                                                                                                           STANDARD;
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109
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                                                                                                        RESULT 4

KV3B HUMAN

KV3B HUMAN

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SEQUENCE
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109 AA

PRELIMINARY;

Q9UL78 HUMAN Q9UL78;

HUMAN

RESULT : Q9UL78 H ID Q9U AC Q9U

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01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18-APR-2006, entry version 2.
Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^{\rm h}{\rm V} kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 MEDLINE=92228746; PubMed=1373487;
Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
"Human combinatorial antibody libraries to hepatitis B surface
                                                                                                                                                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=92202880; PubMed=1552291; DOI=10.1084/jem.175.4.983;
Martin T., Duffy S.F., Cargon D.A., Kipps T.J.;
Martin Evidence for somatic selection of natural autoantibodies.";
J. Exp. Med. 175:983-991(1992).
                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF035036; AAD56272.1; -; mRNA. PIR, A30601; A30601.
PIR, A30601; A30601.
PIR, B30601; B30601.
PIR, B30607; B30607.
PIR, C30601; C30601.
PIR, C30601; C30601.
PIR, C30601; C30601.
PIR, D30607; D30601.
PIR, D30601; D30601.
PIR, D30601; D30601.
PIR, B30601; D30601.
PIR, B30601; D30601.
PIR, B30601; D30601.
PIR, B30601; D30601.
PIR, H30601; H30601.
PIR, H30601; H30601.
PIR, PH0963; PH0964.
PIR, PH0964; PH0964.
PIR, S33988; S33988.
PIR, S33098; S33988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatic mutation.";
Eur. J. Immunol. 23:391-397(1993).
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MEDLINE=93170387; PubMed=8436174;
Wagner S.D., Luzzatto L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-11ke.
InterPro; IPR001399; Ig sub.
InterPro; IPR013106; Ig V-set.
InterPro; IPR001596; Ig_V-set_sub.
                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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SMR; Q9UL78; 1-109
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-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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By similarity.
                                                                                                                                                                                                                                                                          92.8%; Score 518; DB 2; Length 109; 93.5%; Pred. No. 2e-46; ive 2; Mismatches 5; Indels
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Pred, No. 2.2e-45;
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109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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InterPro; IPR003599; Ig-like.

InterPro; IPR003599; Ig-vset.

SMART; SM00409; IG; I.

SMART; SM00406; IG; I.

PROSITE; PSS0835; IG LIKE; I.

Direct protein sequencing; Immunoglobulin domain;

Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. SolMAY-2006, entry version 42. Ig kappa chain V-III region WOL. Homo sapiens (Human).
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                            SMART; SM00409; IG; i.
SMART; SM00406; IGv; i.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
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91.7%;
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Matches 101; Conservative
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SMR; P01623; 1-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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P01623;
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NON TER
SEQUENCE
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STTYSBR
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GO; GO:0016020; C:membrane; IEA.
GO; GO:00130106; P:MHC class I receptor activity; IEA.
GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
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                                                                                                         1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLGWYQQKPGQAPRLLIYGASSRATGIP
                                                   1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
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                                                                                                                                                               61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                            61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                            236 AA.
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY; PRT;
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InterPro; IPR003597; Ig_C1-set.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003599; Ig_sub.
InterPro; IPR013106; Ig_V-set_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, sequence version 1. 27-JUN-2006, entry version 20. Hypothetical protein. Homo sapiens (Human).
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NCBI_TaxID=9606;
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99; Conservative
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Q6PIL8; 21-236.
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QEPILB;
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Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
         1 BIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, Fr4 and B6."; FEBS Lett. 2:301-304(1969).
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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30-MAX-2006, entry version 41.
1g kappa chain V-III region GOL (Rheumatoid factor).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                  DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.1%; Score 503; DB 1; Length 108; 86.1%; Pred. No. 7.5e-45; tive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V-III region
/FTId=PRO 0000059762.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA; 11636 MW; 8BC14FF07A419E3D CRC64;
                                                                                                                                                                                                                                                                                                                                               21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 40. 310-MAY-2006, entry version 86. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11946339; DOI=10.1016/0014-5793(69)80048-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1987, integrated into UniProtKB/Swiss-Prot
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InterPro; IPR007110; Ig-like.
InterPro; IPR003199; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set_sub.
Pfan, PP0768; V-set; I.
SMART; SM00409; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.1<sup>5</sup>
Matches 93, Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin V region.
CHAIN 1 >108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milstein C.;
                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV3G HUMAN
P04206;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                        SWART; SW00409; IG; 1.
SWART; SW04407; IGc1; 1.
SWART; SW00406; IGv; 1.
PROSITE; PSS0035; IG LIKE; 2.
PROSITE; PSS00390; IG MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDIK 129
                                                                                                                                                                                                                                                                                                                                               DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 90.3%; Score 504; DB 2; Length 109; Local Similarity 91.7%; Pred. No. 5.9e-45; les 99; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                               236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
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                                                                                                                                                                                                                                                                                                                                            90.8%; Score 506.5; DB 2, 90.8%; Pred. No. 8.1e-45; iive 5; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA.
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SMR, Q9UL86, 1-109.
InterPro; IPR00710, Ig-like.
InterPro; IPR003599, Ig sub.
InterPro; IPR013106, Ig V. set.
InterPro; IPR013106, Ig V. set.
InterPro; IPR003596, Ig V. set.
FEm; PP07686, V-set; 1.
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PIR; B30607; B30607.
PIR; I30601; I30601.
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Q9UL86;
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SMART; SMO406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
PF07654; C1-set; 1.
PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        99; Conservative
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                                                                                                                               SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
"Amino acid sequence of a light chain variable region of a human
rheumatoid factor of the Wa idiotypic group, in part predicted by its
reactivity with antipeptide antibodies.";
MOI. Immunol. 23:239-244(1986).
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MEDLINE-2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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By similarity.
  Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 500; DB 1; Length 109;
Pred. No. 1.6e-44;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 89 By similarity.
109 109
109 AA; 11830 MW; 9349A5B1D9358BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                         PIR; A01893; K3HUGO.
HSSP; PO1625; 1EK3.
SMR; PO4206; 1-1109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig sub.
InterPro; IPR03599; Ig vab.
InterPro; IPR03596; Ig_V-set.
InterPro; IPR003596; Ig_V-set.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEPUFZ_HUMAN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, sequence version 1. 27-JUN-2006, entry version 21. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 89.6%;
1 Similarity 89.8%;
97; Conservative
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                  Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       >109
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                          PROTEIN SEQUENCE
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GO; GO:0016020; C:membrane; IEA.
GO; GO:00130106; P:MHC Class I receptor activity; IEA.
GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AA; 25521 MW; F33A145A396BA285 CRC64;
                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC016380; AAH16380.1; -; mRNA.
HSSP; P01837; 1KCU.
SMR; Q6PJF2; 21-235.
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QEGMV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2004, sequence version 1.
27-JUN-2006, entry version 21.
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.0%
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Transmembrane
                                               RESULT 13
                                                                       06P5S8
                                                                                               HERE TO THE TOTAL 
                                                                                                         TISSUE-Spleen,

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Wahin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKertan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe, J., Helton B., Ketteman M., Madan A., Rouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Menneration and initial analysis of more than 15,000 full-length human
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GO: 0016020; C:membrane; IEA.
GO: 0010030106; F:MHC class I receptor activity; IEA.
GO: 001030106; F:MHC class I receptor activity; IEA.
GO: 00109881; P:antigen presentation, endogenous antigen; IEA.
GO: 00109885; P:antigen processing, endogenous antigen via . .; IEA.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_sub.
InterPro; IPR003599; Ig_sub.
InterPro; IPR003599; Ig_vset.
InterPro; IPR003596; Ig_V-set.
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SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS500815; IG_LKE; 2.
PROSITE; PS00290; IG_LKE; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.0%; Score 491; DB 2; Length 235; 87.0%; Pred. No. 3.5e-43; Live 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . BC073793; AAH73793.1; -; mRNA. Q6GMV9; 21-235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94; Conservative
                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Alusoner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Wurny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton B., Xetteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Genneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .; IEA.
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

R GO; GO:0019885; P:antigen presentation, endogenous antigen; IEA.

R GO; GO:0019885; P:antigen presentation, endogenous antigen; IEA.

R InterPro; IPR00110; Ig-11ke.

R InterPro; IPR001596; Ig-MHC.

R InterPro; IPR001599; Ig-set.

R InterPro; IPR001599; Ig-set.

R InterPro; IPR001599; Ig-set.

R Pfam; PR07654; C1-set; 1.

R Pfam; PR07656; V-set.

R Pfam; PR07656; V-set.

R Pfam; PR07659; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS002596; IG_LIKE; 2.

R PROSITE; PS002599; IG_LIKE; 2.

R PROSITE; PS002590; IG_MKC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex.class I molecules (By similarity).
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                05-JUL-2004, integrated into UniProtKB/TrEMBL
236 AA.
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HSSP; P01837; 1KCU.
PRT;
                                                                                                                  05-JUL-2004, sequence version 1.
2-JUN-2006, entry version 20.
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Glandular pool- thyroid;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
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QEPSS8 HUMAN
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Search completed: April 25, 2007, 04:06:37 Job time : 73.5254 secs
                                                                 KV3K HUMAN
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SEQUENCE
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                                                                                   21 BIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGATSRATGIP
                                                                                                                                                                                                                                                                                                                                                           "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes.";
Nature 307:77-80(1984).
Nature 307:77-80(1984).
                                                                 1 BIVLTOSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                            Gaps
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                    Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                            ij
                                                                                                           DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-CSFGQGTKLEIK 108
                                                                                                                      Score 481.5; DB 2; Length 236;
Pred. No. 3.5e-42;
9; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V-III region NG9.
/FTId=PRO 0000015174.
By similaTity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%; Score 466; DB 1; Length 100; 94.7%; Pred. No. 5.4e-41; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                     MEDLINE=84093600; PubMed=6419127; DOI=10.1038/307077a0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10729 MW; 5D9AF363CC52632F CRC64;
25773 MW; 953E37BEB4FF5F27 CRC64;
                                                                                                                                                                                                                          21-JUL-1986, sequence version 1.
30-MAY-2006, entry version 44.
10g kappa chin V-III region NG9 precursor (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                             21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensembl; ENSG0000169769; Homo sapiens.
G0; G0:0005576; C:extracellular region; NAS.
G0; G0:0003823; F:antigen binding; NAS.
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR0131906; Ig_V-set.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR013106; Ig_V-set.
                                                                                                                                                                                         100 AA.
                    ch 86.3%; Score 481.5;
1 Similarity 85.3%; Pred. No. 3.5e
93; Conservative 9; Mismatches
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90; Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01894; K3HUNG.
                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01625; 1EEQ.
SMR; P01621; 5-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                               Local Similarity
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                         KV3C_HUMAN
P01621;
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SEQUENCE
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                      Query Match
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                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V-III region IARC/BL41.
/FTId=PRO 0000015178.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86041852, PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.4%; Score 465.5; DB 1; Length 128; 87.0%; Pred. No. 8.1e-41; ive 4; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2.
Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14070 MW; CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                        01-JAN'1988, integrated into UniProtKB/Swiss-Prot. 01-JAN'1988, sequence version 1. 30-MAY-2066, entry version 44. Ig kappa chain V-III region IARC/BL41 precursor.
65 DRFSGSASGTDFTLTISRLEPEDFAVYCQQYGNS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01625; 1EEQ.
SMR; P06311; 21-128.
GO; GO:000575; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z00021; CAA77316.1; -; Genomic_DNA.
PIR; A01899; K3HU41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-1ike.
InterPro; IPR003599; Ig sub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR003596; Ig-V-set.
Pfam; PP07686; V-set; 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 8/...
Local 94; Conservative
                                                                                                                                                                        STANDARD;
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128
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128 1
128 AA;
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Page 9

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GenCore version 6.2.1
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OM protein - protein search, using sw model

April 25, 2007, 04:06:51; Search time 14 Seconds Run on:

(without alignments)
696.311 Million cell updates/sec

US-10-665-383-4 558 Perfect score:

1 EIVLTQSPGTLSLSPGERAT.......CQQYGSSPCSFGQGTKLEIK 108 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\* Issued Patents AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appli	App,	App,	App,	App,	App	App,	App	Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appl	Appl	Appl	App	App	Appl
Ę	42,	16,	16,	16,	16,	6	150	150	150	150	150	150	150	20,	86,	20,	86,	7, 7	14,	65,	80,	80,	34,	178	178,	38,
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΩI	US-08-232-081B-42	US-09-025-769B-16	US-09-490-070A-16	US-09-490-153-16	US-09-490-324-16	US-09-644-668A-9	US-08-488-113B-150	US-08-477-484B-150	US-08-646-360-150	US-08-839-765-150	US-09-136-389-150	US-09-610-838-150	US-09-711-485-150	US-09-456-090A-50	US-09-456-090A-86	US-09-453-234-50	US-09-453-234-86	US-09-644-668A-7	US-09-472-087-14	US-09-472-087-65	US-09-456-090A-80	US-09-453-234-80	US-09-859-053-34	US-09-240-274-178	US-09-848-798-178	US-09-859-053-38
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% Query Match Length	108	109	109	109	109	108	108	108	108	108	108	108	108	226	226	226	226	108	235	235	226	226	236	108	108	236
% Query Match	95.0	94.8	94.8	94.8	94.8	94.6	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.0	94.0	94.0	94.0	93.5	93.4	93.4	92.9	92.9	92.9	95.8	95.8	92.0
Score	530	529	529	529	529	528	525	525	525	525	525	525	525	524.5	524.5	524.5	524.5	522	521	521	518.5	518.5	518.5	518	518	513.5
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Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appli	Appl	Appli	Appl	Appl	Appl							
74,	74,	42,	42,	4,	86,	86,	86,	86,	86,	86,	72,	72,	7	10,	ŝ	17,	14,	14,	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	
US-09-456-090A-74	US-09-453-234-74	US-09-456-090A-42	US-09-453-234-42	US-08-480-774A-4	US-07-634-278-86	US-08-477-728-86	US-08-474-040-86	US-08-487-200-86	US-08-484-537-86	US-09-718-998-86	US-09-456-090A-72	US-09-453-234-72	US-08-635-109-7	US-08-844-215-10	US-08-862-124-5	US-08-862-124-17	US-08-862-124-14	US-08-107-669D-14	
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226	226	226	226	129	108	108	108	108	108	108	226	226	107	107	150	287	304	107	
91.8	91.8	91.7	91.7	91.6	91.0	91.0	91.0	91.0	91.0	91.0	8.06	8.06	7.06	7.06	90.5	90.5	90.5	90.4	
512.5	512.5	511.5	511.5	511	508	208	508	508	508	508	506.5	506.5	206	206	505	505	505	504.5	
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

```
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDBYUKI
APPLICANT: GOMI, HIDBYUKI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-3484
                 . Sequence 42, Application US/08232081B
; Patent No. 5886152
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SYENSON, LECONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-34
TELECOMMUNICATION INFORMATION:
TELEFRA: (703) 205-8000
TELEFRA: (703) 205-8000
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                             CITY: F...
STATE: VA
COUNTRY: USA
T.D: 22040-0747
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
US-08-232-081B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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peptide MOLECULE TYPE: US-08-232-081B-42

95.0%; Score 530; DB 1; Length 108; 94.4%; Pred. No. 1.6e-42; 3, Mismatches Query Match
Best Local Similarity 94.43
Matches 102; Conservative 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60

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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                             ZUDUIN. CONTINC. COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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                                          Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ge, Liming
Moroney, Simon
Plueckhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR AFPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMUNICATION INFORMATION:
TELECHONE: (202) 912-2000
TELEPHONE: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.8%; Score 529; DB 2, 94.4%; Pred. No. 2e-42; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-070A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16:
Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4<sup>†</sup>
Matches 102; Conservative
                             Ilag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-490-153-16
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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                                                  DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: ....
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin BATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-ANG-1995
FILING DATE: 18-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TRLECOMMUTCATION INFORMATION:
TRLECOMMUTCATION:
TRLEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                              Sequence 16, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Moroney, Simon

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

ITLE OF INVENTION: Procein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 529; DB 2;
Pred. No. 2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vuery match
Best Local Similarity 94.4%;
Matches 102; Conservative
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TYPE: amino acid
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MOLECULE TYPE: protein
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US-09-490-070A-16
                                                                                                                                                                           RESULT 2
US-09-025-769B-16
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ORGANISM: Homo sapiens
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Best Local Simi
Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                           CURRENT ITES: Floppy diba
COMPUTE: Floppy diba
COMPUTE: Floppy diba
COMPUTE: Floppy diba
COMPUTE: Exerciting SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1996
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 529; DB 2; Length 109;
Pred. No. 2e-42;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuu, Andreas
TITLE OF INVBITION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/490,324
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 94.4
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'ELEFAX:
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US-09-490-324-16
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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APPLICANT: Halk, Edward L.
APPLICANT: Halk, Edward L.
APPLICANT: Lonberg, Nils
TAPLICANT: Lonberg, Nils
APPLICANT: Medarex, Inc.
TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
FILE REFERENCE: 014643-010510US
CURRENT APPLICATION NUMBER: US/09/644,668A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/150,452
PRIOR APPLICATION NUMBER: US 60/150,452
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 94.4%; Score 529; DB 2; Length 109; Similarity 94.4%; Pred. No. 2e-42; Conservative 3; Mismatches 3; Indels
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                                                       APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  NAME: James P. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-324-16
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)596-9000
TELEFAR: (212)596-9090
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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RESULT 8
10S-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756699
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STRANDEDNESS: double
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                                                                           Sequence 150, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinks, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                        E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: bau PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA: 12-MAY-1993
PRIOR APPLICATION DATA: 12-MAY-1993
PRIOR APPLICATION DATA: 09-DEC-1992
PRIOR APPLICATION DATA: 09-DEC-1992
PRIOR APPLICATION DATA: 09-DEC-1992
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 31,102
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 312/707-8899
TELEFAX: 312/707-889
INFORMATION FOR SEG 1D NO: 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 amino acids
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STREET: Soc
CITY: Chicago
CTATE: Illinois
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                           RESULT 7
US-08-488-113B-150
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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
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94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASS!FICATION NUMBER: US 08/425,336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-APY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: US 07/988,430
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MCNIcholas, Janec M.
REGISTRATION NUMBER: 32,918
REGISCOMMUNICATION NUMBER: 11022US07/200-70.P3.C2A
TELEPHONE: 312/707-8889
TELEFRAX: 312/707-8889
TELEFRAX: 512/707-8155
INFORMATION FOR SEQ ID NO: 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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                   Sequence 150, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STRIE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSITEATION: 530
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 10-MAY-1993
FRICK APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-MAY-1993
FRICK APPLICATION NUMBER: US 07/981,707
FILING DATE: 19-JUN-1992
FRICK APPLICATION NUMBER: US 07/901,707
FILING DATE: 10-MAY-1991
APPLICATION NUMBER: US 07/97,567
FILING DATE: 19-MAY-1991
APPLICATION NUMBER: US 07/97,567
FILING DATE: 10-NOV-1991
APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-8889
TELEFPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 amino acids
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Best Local Similarity 94.45
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
US-08-646-360-150
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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                                                                             APPLICANT: BAILOR:
APPLICANT: BAILOR:
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Froteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSE: MACANDENCE ADDRESS:
ADDRESSE: MACANDENCE ADDRESS:
CITY: Chicago
STREET: SOO West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DRFSGSGSGTDFTLTISRLEPGDFAVYCQQYGSSPXTFGQGTKVEIK 108
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94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25
SUSTWARE: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 13-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-8899
TELEEPAN: 312/707-8899
TELEEPAN: 312/707-8899
TELEEPAN: 312/707-8155
Sequence 150, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
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RESULT 11 US-09-136-389-150

RESULT 10

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Sequence 150, Application US/09610838 Patent No. 6376217 GENERAL INFORMATION:
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US-09-610-838-150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                         GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDREWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.1%; Score 525; DB 2; Length 108; 94.4%; Pred. No. 4.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLILING WATE:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRICE BAPEL AND NUMBER: 08/646,360

PRILING DATE: 13-MAY-1996

APPLICATION NUMBER: DCT/US94/05348

FILING DATE: 12-MAY-1994

PRICE BAPEL CATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 08-DEC-1992

PRICE CATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRICE OF DEC-1992

PRICE OF DEC-1992

PRICE SPELICATION DATA: US 07/981,707

FILING DATE: 08-DEC-1992

PRICE SPELICATION NUMBER: US 07/901,707

FILING DATE: 08-DEC-1991

APPLICATION NUMBER: US 07/787,567

FILING DATE: 08-NOV-1991

APPLICATION NUMBER: US 07/787,567

FILING DATE: 08-NOV-1991

ATORNEY/AGENT INFORMATION:

RECEISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELEPONE: 312/707-9155

TELEPANE: 312/707-9155

TELEPANE: 650 388-1248

INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
Sequence 150, Application US/09136389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.44
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-136-389-150
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                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                  Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAURENT APPLICATION DATA:
APPLICATION UNDER: US/09/610,838
FILING DATE: 06-JUL-2000
                                                                                                                   STREE: MCANDREWS. Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
GTY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA APPLICATION DATA APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,918
REGESTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
TELECOMMUNICATION INFORMATION:
TELECHONE: 312/707-9889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-NG-1998
FILING DATE: 13-M2-1996
FILING DATE: 13-M2-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
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Search completed: April 25, 2007, 04:08:33 Job time : 14.5763 secs
IS-09-456-090A-50
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 50
LENGIH: 226
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                        Sequence 150, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 4.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
                                                                                                                                                                                                                                                                             3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.1%; Score 525; DB Best Local Similarity 94.4%; Pred. No. 4.7e Matches 102; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INPORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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RESULT 13
US-09-711-485-150
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1 BIVLTOSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Pred. No. 1.2e-41;
1; Mismatches 3; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86, Application US/09456090A

Patent No. 6680209

GERERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jef
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFRENCE: 020015-0002000US
CURRENT APPLICATION NUMBER: US/09/456,090A

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 226;
                                                                                                  APPLICANT: Valkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonbery, Nils
FITILE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.2e-41;
1; Mismatches 3
Sequence 50, Application US/09456090A
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Best Local Similarity 95.4%;
Matches 104; Conservative
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95.4%;
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SEQ ID NO 86
LENGTH: 226
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Best Local Similarity 95.4<sup>†</sup>
Matches 104<sup>‡</sup>, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
COTHER INFORMATION: M1-23L
US-09-456-090A-50
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OTHER INFORMATION: M2-33L
                   Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
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; ORGANISM: homo sapiens
US-10-041-860-49
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Sequence 225, App
Sequence 259, App
Sequence 375, App
Sequence 11, Appl
Sequence 116, Appl
Sequence 123, App
Sequence 123, App
Sequence 123, App
Sequence 27, Appl
Sequence 121, App
Sequence 161, App
Sequence 161, App
Sequence 161, App
Sequence 161, App
Sequence 122, App
Sequence 122, App
Sequence 804, App
Sequence 804, App
Sequence 805, App
                                                                                 April 25, 2007, 04:18:18; Search time 40 Seconds (without alignments) 1251.741 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  US-10-665-383-4
558
1 EIVLTQSPGTLSLSPGERAT.......CQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
           GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-041-860-49
US-10-041-860-255
US-10-041-860-255
US-10-041-860-255
US-10-041-860-375
US-10-651-84
US-10-891-658-84
US-10-891-658-131
US-10-991-658-131
US-10-991-658-131
US-10-90-901-13
US-10-90-901-13
US-10-90-762-156
US-10-737-290-161
US-10-737-290-162
US-10-737-290-163
US-11-000-463-805
US-11-000-463-805
US-11-000-463-805
US-11-000-463-805
US-11-000-463-807
US-11-000-463-807
US-11-000-463-807
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                                                                                                                                                                                                                                                                                                                                                             Applications AA Main:*
                                                                                                                                                                                                                         2097797 seqs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                               Published
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                                                                                                                                                Perfect score:
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Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 112, Appli
Sequence 112, Appli
Sequence 210, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 163, Appli
Sequence 150, Appli
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                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10041860
Sequence 49, Application US/10041860
Sequence 49, Application No. US20030157109A1
SEPLECANT: OCCAVAININI
APPLICANT: COCYVALANI JOSE R.F.
APPLICANT: VANG, Xiao-Chi
APPLICANT: VANG, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Brancine
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/202-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 558; DB 4; Length 1
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 108; Conservative 0; Mismatches 0; Indels
US-10-684-109-21

US-10-84-939-16

US-11-040-846-9

US-11-056-825-8

US-11-056-825-4

US-10-318-366-4

US-10-318-366-4

US-10-318-36-112

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-938-353-110

US-10-171-243-150

US-10-177-243-150

US-10-177-243-150
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APPLICANT: Corvalan, Jose R.F.; APPLICANT: Corvalan, Jose R.F.; APPLICANT: Feng, Xiao-Chi; APPLICANT: Yeng, Xiao-Dong; APPLICANT: Chen, Francine; APPLICANT: Gazit, Gadi
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Jia, Xiao-Chi
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 558; DB 4; Length 108; 100.0%; Pred. No. 5e-40;
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazi, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bazabeh, Blinyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 558; DB 4; 100.0%; Pred. No. 5e-40; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 100.0
Matches 108; Conservative
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Best Local Similarity 100.'
Matches 108; Conservative
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US-10-041-860-259
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; ORGANISM: homo sapiens
US-10-041-860-225
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APPLICANT:
APPLICANT:
APPLICANT:
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 108;
                                                                               APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh Blunyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: THEREOF
FILE REFREENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 550; DB 4; Length 10
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 100; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REPERENCE: ADGRIX: 0.52
CURRENT APPLICATION NUMBER: 0.16
PRIOR PILING DATE: 2003-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 108
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Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 108; Conservative 0; Mismatches 0;
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Publication No. US20040141969A1;
GENERAL INFORMATION:
APPLICANT: Floege, Juergen
APPLICANT: ReyC, Bruce
APPLICANT: LAROCHALL, William
APPLICANT: LAROCHALL, William
APPLICANT: Lichenstein, Henri
Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-375
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ORGANISM: homo sapiens
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US-10-891-658-84

RESULT 6

Sequence 375, Application US/10041860 Publication No. US20030157109A1 GENERAL INPORMATION: APPLICANT: Corvalan, Jose R.F.

US-10-041-860-375

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21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
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Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Grads, Jean
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
ITILE OF INVENTION: (A IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT APPLICATION NUMBER: 60/337275
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DRFSGSGSGTDFTLTISKLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
    61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGQGTKLEIK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128;
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Pred. No. 5.4e-38;
1; Mismatches 3
                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION:
FILE REPERENCE: ABX-PF5
CURRENT APPLICATION:
FILE REPERENCE: ABX-PF5
CURRENT APPLICATION NUMBER: US/10/910,901
CURRENT APPLICATION NUMBER: US 60/492,432
PRIOR FILING DATE: 2004-08-03
PRIOR FILING DATE: 2003-08-04
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 18
LENGTH: 128
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 156
LENGTH: 108
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ilarity 96.3%;
Conservative
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US-10-910-901-18
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Best Local Similarity
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                                                                                            APPLICANT: Treanor, James
APPLICANT: Treanor, James
APPLICANT: Treanor, James
APPLICANT: Inoue, Heather
APPLICANT: Zhang, Tie J.
APPLICANT: Zhang, Tie J.
APPLICANT: Martin, Frank
TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: 02-1240
CURRENT APPLICATION NUMBER: US/10/891,658
PRIOR APPLICATION NUMBER: US 60/487,431
PRIOR APPLICATION NUMBER: US 60/487,431
PRIOR PILING DATE: 2003-07-15
PRIOR FILING DATE: 2003-07-15
SOFTHARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Treanor, James
APPLICANT: Huang, Halchun
APPLICANT: Huang, Halchun
APPLICANT: Zhang, Tie J.
APPLICANT: Zhang, Tie J.
APPLICANT: Prank
Martin, Frank
TITLE OF INVENTION: Inhibitors
FILE REPERENCE: 02-1240
CURRENT APPLICATION NMERR: US/10/891,658
CURRENT FILING DATE: 2004-07-15
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Pred. No. 4.5e-38;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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Pred. No. 4.5e-38;
1; Mismatches 3;
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PRIOR APPLICATION NUMBER: US 60/487,431
PRIOR FILING DATE: 2003-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 131, Application US/10891658; Publication No. US20050074821A1; GENERAL INFORMATION:
Sequence 84, Application US/10891658
Publication No. US20050074821A1
GENERAL INFORMATION:
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96.3%;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 131
LENCTH: 108
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Matches 104; Conservative
                                                                          APPLICANT: Kenneth, Wild
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapien
US-10-891-658-131
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US-10-891-658-131
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, OTHER INFORMATION: antibody light chain variable region US-10-307-724-123
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Sequence 123, Application US/10737290
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Sequence 27, Application US/10725962
Publication No. US20050013809A1
GENERAL INFORMATION:
APPLICANT: Samuel M. Owens
APPLICANT: Frank I. Carroll
APPLICANT: Philip Abraham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
                                                                                   Query Match
Best Local Similarity 95.4%;
Matches 103; Conservative
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Pred. No. 8.1e-38;
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US-10-307-724-123

i Sequence 123, Application US/1030724

i Publication No. US20030232972A1

i GENERAL INFORMATION:
   APPLICANT: Bowdish, Katherine S.
   APPLICANT: Brederickson, Shana
   APPLICANT: Renshaw, Mark
   ITIER OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
   FILE REFERENCE: 1087-22ip
   CURRENT FILING DATE: 2002-12-02
   PRIOR APPLICATION NUMBER: US 60/291,448
   PRIOR APPLICATION NUMBER: US 60/294,068
   PRIOR FILING DATE: 2000-12-05
   PRIOR FILING DATE: 2001-05-04
   PRIOR PILING DATE: 2001-05-04
   PRIOR PILING DATE: 2001-05-05
   NUMBER OF SEQ ID NOS: 134
   SOFTWARE: PatentIn version 3.2
   SEQ ID NO 123
   SEQ ID NO 123
                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: YOSHIDA, Hitoshi
APPLICANT: POCE, Walker, R.
APPLICANT: FORCE, Walker, R.
APPLICANT: FORCE, Walker, R.
APPLICANT: TAKAHASHI, Nobuaki
TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
FILE REFERENCE: 021286-0306473
CURRENT APPLICATION NUMBER: 2003-11-13
CURRENT PILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR PELICATION NUMBER: JP2001/142482
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                         Sequence 46, Application US/10693629
Publication No. US20040120948A1
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95.4%;
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ORGANISM: artificial sequence
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ORGANISM: Homo sapiens
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Best Local Similarity
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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Length 108;
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| PUDICALION NO. USZOWAOZSZAZAI
| APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
| APPLICANT: Renshaw, Mark
| APPLICANT: Orencia, Cecilia |
| TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES |
| FILE REFERENCE: 1087-2 CIP III |
| CURRENT PILING DATE: 2003-12-15 |
| PRIOR APPLICATION NUMBER: US 10/452,590 |
| PRIOR APPLICATION NUMBER: US 10/307,724 |
| PRIOR APPLICATION NUMBER: US 00/006,593 |
| PRIOR PILING DATE: 2001-12-05 |
| PRIOR APPLICATION NUMBER: US 60/251,448 |
| PRIOR FILING DATE: 2000-12-05 |
| PRIOR PILING DATE: 2001-05-04 |
| PRIOR FILING DATE: 2001-05-04 |
| PRIOR FILING DATE: 2001-05-29 |
| NUMBER: OF SEQ ID NOS: 193 |
| SOFTWARE: PatentIn Version 3.2 |
| LENGTH: 108 |
| LENGTH: 108 |
| LENGTH: 108 |
| LENGTH: 108 |
| LENGTH: LOBERT |
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Score 532; DB 4;
Pred. No. 8.2e-38;
2; Mismatches 3
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Publication No. US20050106140A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lancaster. Joanne Sloan
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: X15450 - National Stage
CURRENT APPLICATION NUMBER: US/10/506,743
FRICA PAPLICATION NUMBER: 60/367,054
PRIOR PILING DATE: 2004-09-03
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Pred. No. 8.3e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
APPLICANT: Mary Haak-Frendscho
APPLICANT: Xiao Feng
TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
FILE REPERENCE: ABGENIX.071A
CURRENT APPLICATION NUMBER: US/10/725,962
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430717
PRIOR APPLICATION NUMBER: 60/430717
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040253242A1
GENERAL INFORMATION:
APPLICANT: Browdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Crencia, Cecilia
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                  Query Match 95.3%; Score 532; DB Best Local Similarity 95.4%; Pred. No. 8.3e Matches 103; Conservative 2; Mismatches
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Best Local Similarity 95.49
Matches 103, Conservative
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LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-725-962-27
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                                                                                                                                                                                                                      SEQ ID NO 27
LENGTH: 109
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Search completed: April 25, 2007, 04:22:51 Job time : 39.9661 secs

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Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3

Sequence 68, A Sequence 178, Sequence 48, A Sequence 296,

Sequence 16, 1 Sequence 87, 1 Sequence 44, 1 Sequence 10, 1

Sequence Sequence 3

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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SEQUENCE 49, Application US/11109181

FUBLICATION NO. US20060293506A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Peng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Chen, Francine

APPLICANT: Weber, Richard

APPLICANT: OF AN UNBER: US/10/041,860

PRIOR FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FREESE for Windows Version 4.0

SEQ ID NO 49

LENGTH: 108

TYPE: PRT
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100.0%; Pred. No. 5.1e-44;
ative 0; Mismatches 0;
US-11-396-495-5

US-11-433-924-176

US-11-520-312-16

US-11-396-495-13

US-11-396-495-13

US-11-398-696-14

US-11-588-696-14

US-11-517-530-28

US-11-517-530-28

US-11-517-530-68

US-11-317-530-16

US-11-333-924-296

US-11-317-939-87

US-11-375-221-44

US-11-375-221-44

US-11-375-221-44

US-11-317-939-87

US-11-375-221-44

US-11-317-939-87

US-11-317-939-87
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Sequence 225, Application US/11109181

Publication No. US20060293506A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 100.
Matches 108; Conservative
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US-11-109-181-49
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132, App
46, Appli
132, App
628, Appl
102, App
23, Appl
24, Appl
60, Appl
60, Appli
114, Appli
115, Appli
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Sequence 259, App
Sequence 375, App
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                                                                                                                                                                                                                  April 25, 2007, 04:23:02 ; Search time 42 Seconds (without alignments) 533.620 Million cell updates/sec
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FEMC_Celerra_SIDS3/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/USO7_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/NCT_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/USI0_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/USI0_NEW_PUB.pep:*
FEMC_Celerra_SIDS3/prodata/1/pubpaa/USI0_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                            US-10-665-383-4
558
1 BIVLTQSPGTLSLSPGERAT......CQQYGSSPCSFGQGTKLBIK 108
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                                   GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-11-109-181-255

US-11-109-181-255

US-11-109-181-375

US-11-517-530-8

US-11-517-530-8

US-11-517-530-132

US-11-517-530-132

US-11-517-530-132

US-11-517-530-127

US-11-131-939-628

US-11-1009-410-22

US-11-009-410-22

US-11-009-410-22

US-11-109-410-24

US-11-154-4

US-11-375-221-60

US-11-375-221-60

US-11-375-221-60

US-11-375-221-114

US-11-375-221-113

US-11-375-221-60

US-11-375-221-60

US-11-375-221-60

US-11-375-221-60

US-11-375-221-60

US-11-375-221-113

US-11-317-330-135

US-11-317-330-135

US-11-11-939-659

US-11-145-131A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA New:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Result No.

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ORGANISM: Human
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100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UK-11-10-181-259

; Sequence 259, Application US/11109181
; Publication Vo. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Grain, Xiao-Chi
; APPLICANT: Yang, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gazit, Gadi
; APPLICANT: Rend, Rancine
; APPLICANT: Rebeh, Binyam
; TITLE OF INVENTION: ANTHRODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION UNDER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
            APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: APTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR PILING DATE: 2002-01-07
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-225
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ORGANISM: homo sapiens
Feng, Xiao
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LENGTH: 108
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Sequence 8, Application US/11517530

Sequence 8, Application US/11517530

Publication No. US20070065444A1

GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Amagen Fremont Inc.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
FILE REFERENCE: ABX-PF9 PROV
CURRENT APPLICANTION NUMBER: US/11/517,530

CURRENT FILING DATE: 2006-09-06
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
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                                                                                                                                                                                                              APPLICANT: Gazir, Gadi
APPLICANT: Gazir, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
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100.0%; Pred. No. 5.1e-44;
trive 0; Mismatches 0;
Sequence 375, Application US/11109181 Publication No. US20060293506A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 96.3
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 108; Conservative
                                                                                                                                                                                                   Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-375
                                                                                                                                              Feng, Xiao
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Sequence 132, Applic
Publication No. US20
GENERAL INFORMATION:
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APPLICANT: Kellermann, Sirid-Aimee
APPLICANT: Foord, Orit
APPLICANT: Floord, Orit
APPLICANT: Belouski, Shelley Sims
APPLICANT: Belouski, Shelley Sims
APPLICANT: Belouski, Shelley Sims
APPLICANT: Green, Larry L.
TITLE OF INVENTION: URRY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
TITLE OF INVENTION: OTHER DISORDERS
TITLE OF INVENTION: OTHER DISORDERS
FILE REFERENCE: ABGENIX:120A
CURRENT FILING DATE: 2006-05-12
PRIOR PELLING DATE: 2006-05-16
PRIOR FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 419
SEQ ID NO 180
SEQ ID NO 180
LENGTH: 108
                                                               Sequence 4, Application US/11517530
Publication No. US2007006544A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: AMON Fremont Inc.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
FILE REPRENCE: ABX-PF9 BROV
CURRENT APPLICATION NUMBER: US/11/517,530
CURRENT FILING DATE: 2006-09-06
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVITQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 538; DB 7; Length 215;
Pred. No. 7e-42;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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US-11-431-924-180
US-11-431-924-180
Sequence 180, Application US/11433924
Publication No. US20060286112A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.4%;
96.3%;
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Matches 104; Conservative
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ORGANISM: Homo sapiens
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                                                JS-11-517-530-4
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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RESULT

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APPLICANT: Pfizer Inc.
APPLICANT: Pfizer Inc.
APPLICANT: Premont Inc.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
FILE REPERBUCE: ABX-PF9 PROV
CURRENT APPLICATION NUMBER: US/11/517,530
CURRENT FILING DATE: 2006-09-06
SUUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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Pred. No. 1.2e-41;
2; Mismatches 3; Indels
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APPLICANT: KIRIN BEER KABUSHKI KAISHA
APPLICANT: WIKAYAMA, Toshifumi
APPLICANT: YOSHIDA, Hitoshi
APPLICANT: FORCE, Walker, R.
APPLICANT: TAKAHASHI, Nobuaki
TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
FILE REFERENCE: 021286-0389823
CURRENT PILLING DATE: 2006-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1e-41;
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PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: JP2001/310535
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 66
SOFWWARE: PATCHIN VEY: 2.1
SEQ ID NO 46
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PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: PCT/US01/13672
Application US/11517530 . US20070065444A1
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Publication No. US20070077242A1
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95.4%;
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Best Local Similarity 95.4%;
Matches 103; Conservative
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Best Local Similarity
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ORGANISM: Human
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Sequence 102, Application US/11517530
Publication No. US2007006544A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
FILE REPRENCE: ABA-FPP PROV
CURRENT APPLICATION NUMBER: US/11/517,530
CURRENT PILING DATE: 2006-09-06
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 102
LENGTH: 215
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; Sequence 23, Application US/11009410
; Publication No. US20070014724A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Denise
; APPLICANT: Williams, Denise
; APPLICANT: Williams, Denise
; APPLICANT: King, David
; APPLICANT: King, David
; APPLICANT: King, David
; APPLICANT: King, David
; TITLE OF INVERTION: INTERFERON ALPHA ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1200696-US1
; CURRENT APPLICATION NUMBER: US/11/009,410
; CURRENT APPLICATION NUMBER: 60/528,757
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 37
; SGQ ID NO 23
; LEMGTH: 108
; TEMBER OF SEQ ID NOS: 37
; CONTWARE: PALENTIN VERSION 3.2
; ERGITH: 108
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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                             61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
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Pred. No. 2.5e-41;
2; Mismatches 3;
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Best Local Similarity 95.4%;
Matches 103; Conservative
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Best Local Similarity
Matches 103; Conserv
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ORGANISM: Human
                                                                                                                                                      US-11-517-530-102
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                                                                                                                                                                            Sequence 127, Application US/11517530
Publication No. US20070065444A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Amgen Fremont Inc.
TITLE OP INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
FILE REPERBINGS: ABX-PF9 ROV
CURRENT APPLICATION NUMBER: US/11/517,530
CURRENT APPLICATION NOWER: 2066-09-06
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.3
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     DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 95.3%; Score 532; DB 7; Length 108; Similarity 95.4%; Pred. No. 1.3e-41; 03; Conservative 2; Mismatches 3; Indels
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APPLICANT: Zhou, Qing
APPLICANT: Zhou, Qing
APPLICANT: Keyt, Bruce A.
APPLICANT: Bmery, Xiao-Dong
APPLICANT: Blakey, David C.
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: ABXAZ.002A
FILE REPERENCE: ABXAZ.002A
CURRENT APPLICATION NUMBER: US/11/311,939
CURRENT PILING DATE: 2005-12-19
FRIOR APPLICATION NUMBER: US 60/638,354
FRIOR APPLICATION NUMBER: US 60/638,354
FRIOR APPLICATION NUMBER: US 60/638,354
FRIOR PLING DATE: 2006-12-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20060246071A1
GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-11-311-939-628
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Best Local Simi
Matches 103;
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LENGTH: 108
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us-10-665-383-4.rapbn
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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Sequence 22, Application US/11009410

| Publication No. US20070014724A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Denise
| APPLICANT: Williams, Denise
| APPLICANT: Williams, Denise
| APPLICANT: King, David
| APPLICANT: King, David
| TITLE OF INVENTION: INVERFENCE ADVICESTION OF THE REPERENCE: US/11/009,410
| TITLE OF INVENTION: INVERFENCE IS/11/009,410
| TITLE OF INVENTION: INVERFENCE IS/11/009,410
| TITLE OF INVENTION: INVENTION: USES: STOLE APPLICATION NUMBER: US/11/009,410
| CURRENT APPLICATION NUMBER: 06/528,757
| PRIOR FILING DATE: 2004-12-10
| WUMBER OF SEQ ID NOS: 37
| SEQ ID NO 22
| LENGTH: 108
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| Publication No. US20070014724A1
| GENERAL INFORMATION
| APPLICANT: Williams, Denise
| APPLICANT: Williams, Denise
| APPLICANT: Cardarelli, Josephine M. APPLICANT: King, David
| APPLICANT: Rassmore, David
| TITLE OF INVENTION: INTERPENCE AND THEIR USES
| TITLE OF INVENTION: INTERPENCE AND THEIR USES
| CURRENT APPLICATION NUMBER: US/11/009,410
| CURRENT APPLICATION NUMBER: US/11/009,410
| PRIOR PTILING DATE: 2004-12-10
| PRIOR PTILING DATE: 2003-12-10
| NUMBER OF SEQ ID NOS: 37
| SOFTWARE: PatentIn version 3.2
| LENGTH: 108
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Pred. No. 2.9e-41;
3; Mismatches 3; Indels
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Pred. No. 2.9e-41;
3; Mismatches 3; Indels
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Best Local Similarity 94.4%;
Matches 102; Conservative 3
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Best Local Similarity 94.4%;
Matches 102; Conservative
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ORGANISM: Homo sapiens
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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIK 108

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Search completed: April 25, 2007, 04:27:44 Job time : 41.6441 secs

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April 25, 2007, 03:54:56; Search time 109 Seconds (without alignments) 564.248 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Adk18597 Anti-huma	Adk18870 Anti-huma	Adk18812 Anti-huma	Adk18775 Anti-huma	Adl25412 Human mAb	Adk18925 Anti-huma	Adk18780 Anti-huma	Adk18616 Anti-huma	Adk18817 Anti-huma	Adl25448 Human mAb	Adk18864 Anti-huma	_	Adk18777 Anti-huma	Adl25408 Human mAb	Adk18778 Anti-huma	Adk18613 Anti-huma	Adk18815 Anti-huma	Adl25464 Human mAb	Adk18614 Anti-huma	Adk18779 Anti-huma	Adk18919 Anti-huma	Adk18816 Anti-huma
SUMMARIES	ADK18597	ADK18870	ADK18812	ADK18775	ADL25412	ADK18925	ADK18780	ADK18616	ADK18817	ADL25448	ADK18864	ADK18595	ADK18777	ADL25408	ADK18778	ADK18613	ADK18815	ADL25464	ADK18614	ADK18779	ADK18919	ADK18816
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8 ADL25444 6 ABR55829 10 AEG17553 10 AEG17553	7 ADK18814 10 AEH94456 10 AEK98538 7 ADK18620	7 ADK18818 7 ADK18781 7 ADK18936	8 ADL25456 7 ADK18776 7 ADK18948 7 ADK18624	7 ADK18813 8 ADL25392 10 AEK98534 2 AAW88464	9 AED87298 10 AEH94503 10 AEK98141 2 AAY34302
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22 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	27 28 30 30	33 33 33	34 35 37	38 39 40 41	4 4 4 4 5 6 4 6

## ALIGNMENTS

antiinflammatory; immunomodulator; cytostatic; gene therapy Gazit G, Anti-human PDGF-D antibody heavy chain protein sequence. Chen F, Yang X, ADK18597 standard; protein; 126 AA. Feng X, 06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860. (first entry) Corvalan JRF, Jia X, (ABGE-) ABGENIX INC WO2003057857-A2. sapiens. 06-MAY-2004 17-JUL-2003 Bezabeh B; ADK18597; Ношо RESULT 1 ADK18597 

Weber R;

WPI; 2003-587119/55.

growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 21; 255pp; English

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.

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                                                          Score 666; DB 7;
Pred. No. 2.8e-53;
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Matches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK18812;
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121 TVTVSS 126

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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY

100.0%; Score 666; DB 7; Length 126; 100.0%; Pred. No. 2.8e-53; ive 0; Mismatches 0; Indels

Conservative

Similarity

Best Local Sim: Matches 126;

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Query Match

ADK1877

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binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:
(1) a method of detecting nephritis; (2) a method of treating nephritis;
of treating mesangial cell proliferation; and (4) a method of trial proliferation; and (4) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene thearpy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclomal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an antibody or its binding fragment that
                                                                                                                                           antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating
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                                                                                                   Human mAb 1.19 heavy chain variable region protein SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 666; DB 8; Best Local Similarity 100.0%; Pred. No. 2.8e-53; Matches 126; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 gene therapy; human; monoclonal antibody; mAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 22; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keyt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK18925 standard; protein; 126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-2002; 2002US-0411137P
                                                  17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-269881/25.
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N-PSDB; ADL25411
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                                                                                                                                                                                                                                                                                                                                                    WO2004024098-A2
                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nephritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for stading various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEKZ93 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gazit G,
                                                                                                                                                                                                                                                                                                  Anti-human PDGP-D antibody protein related sequence #1.
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100.0%; Pred. No. 2.8e-53;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 199; 255pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL25412 standard; protein; 126 AA.
                                                                                                                                                   ADK18775 standard; protein; 126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-2003; 2003WO-US000398.
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                                                                                                                                                                                                                                                      (first entry)
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Matches 126; Conservative
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121 TVTVSS 126
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                                                                                                                                                                                                      ADK18775;
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Lichenstein H;

Larochelle WJ,

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RESULT 5 ADL25412 ID ADL2 XX

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Gaps

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Length 126; Indels

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                                                                                                                                                                                                                                                                                  Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human monoclonal antibody that binds to
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                                                                                                                                                                                                                                                                                                                                                   New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                  antiinflammatory; immunomodulator; cytostatic; gene therapy
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                                                                                                                                                                                                                                                                                  Gazit G,
                                                       Anti-human PDGF-D antibody protein related seguence #151.
                                                                                                                                                                                                                                                                                Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 349; 255pp; English
                                                                                                                                                                                                                                                                                  Yang X,
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                                                                                                                                                                                                                         07-JAN-2002; 2002US-00041860
                             (first entry)
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                                                                                                                                                                                                                                                                                                                          WPI; 2003-587119/55.
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                                                                                                              Homo sapiens
                             06-MAY-2004
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 ADK18925
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antiinflammatory; immunomodulator; cytostatic; gene therapy.

Anti-human PDGF-D antibody protein related sequence #6.

06-MAY-2004

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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVTATDYYYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                        are useful for
                                                                                                                                                                                                                                                                                                                                                     treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleat caids and polypeptides are useful for useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188. Or 99 arrising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                           invention relates to a human monoclonal antibody that binds to
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                                                                                                                                                                            Gazit
                                                                                                                                                                            Chen F,
                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 204; 255pp; English
                                                                                                                                                                            Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK18616 standard; protein; 126 AA.
                                                                                                                                                                            Feng X,
                                                                                    06-JAN-2003; 2003WO-US000398.
                                                                                                                   07-JAN-2002; 2002US-00041860
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                           WO2003057857-A2.
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                                                                                                                                                                          Corvalan JRF,
Homo sapiens.
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                                                        17-JUL-2003
                                                                                                                                                                                           Bezabeh B;
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(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.
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N-PSDB; ADL25447.
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                                                                                                                                                                                                                                                                                                                                                          Sequence 126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                            The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunty and cancer. The PDGF-D nucleic acids and polypebtides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when
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                                                                               Weber R;
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                                                                                                                                                                          New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.8%; Score 605; DB 7; Length 126;
89.7%; Pred. No. 1.1e-47;
.ive 6; Mismatches 7; Indels
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                                                                               Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human PDGF-D antibody protein related sequence #43.
                                                                               Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen F,
                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 40; 255pp; English
                                                                               Yang X,
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                                                                               Feng X,
07-JAN-2002; 2002US-00041860
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Best Local Similarity 89.7
Matches 113; Conservative
                                                                               Jia X,
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                                                                                                                                     WPI; 2003-587119/55.
                                      (ABGE-) ABGENIX INC
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                                                                               Corvalan JRF,
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                                                                                                   Bezabeh B;
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lichenstein H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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growth
human
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New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.8%; Score 605; DB 7; Length 126; 89.7%; Pred. No. 1.1e-47; rive 6; Mismatches 7; Indels
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                                                                                                                                                             Disclosure; SEQ ID NO 241; 255pp; English
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Matches 113; Conservative
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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

(1) a method of detecting nephritis; (2) a method of treating nephritis;

(3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating meaning an proliferative glomerulonephritis; rhe antibody has nephrotropic, antiinflammatory, dermatchlogical, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerullonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVTATDYYYGMDVWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTRNTS1STAYMELSSLRSEDTAVYYCARDVM1TFGGVIVHYGMDVWGQGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-human PDGF-D antibody protein related sequence #90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen F,
                                                                                                                                                                                                                                                                                                                                 Score 605; DB 8;
Pred. No. 1.1e-47;
                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                SEQ ID NO 58; 115pp; English
                                                                                                                                                                                                                                                              exemplification of the present invention
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                 Sequence 126 AA;
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                                Disclosure;
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nephritis
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platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
                                                                    generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating chronic and recurrent human diseases, such as inflammation, treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The POGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0, 99 arising in the conditioned medium obtained when HBK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
                  treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D mucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
                                                                                                                                                                                                                                                                                                                                                              61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT
                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                  Length 126;
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                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-human PDGF-D antibody heavy chain protein sequence.
                                                                                                                                                                                                                Score 604; DB 7; L Pred. No. 1.4e-47; 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 19; 255pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK18595 standard; protein; 126 AA.
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                                                                                                                                                                                                                Query Match 90.7%;
Best Local Similarity 91.3%;
Matches 115; Conservative
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Weber R;

Gazit G,

growth human

The invention relates to a human monoclonal antibody that binds to

Disclosure; SEQ ID NO 288; 255pp; English.

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                                                                                                                                                                                          61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT
                                                                                                                                                                           AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT
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                                                          Length 126
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 to a protein used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen F,
                                                         Score 604; DB 7;
Pred. No. 1.4e-47;
3; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                       ADK18777 standard; protein; 126 AA.
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                                                       90.7%;
91.3%;
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                                                      Query Match
Best Local Similarity 91.3
Matches 115; Conservative
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 sequence corresponds
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TVTVSS 126
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                              Sequence 126 AA;
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(1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antihilammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                9
                                                                                                                                                                                                                                                                                                                                                                                           antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet derived
for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larochelle WJ, Lichenstein H;
                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMPNSGNTGY
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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llarity 91.3%; Pred. No. 1.4e-47;
Conservative 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an antibody or its binding fragment factor-DD (PDGF-DD) for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
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                                                                                                                                                                                                                                                         ADL25408 standard; protein; 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L6-SEP-2003; 2003WO-US029414.
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                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 115; Conserval
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                                                                                                                                       121 TVTVSS 126
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growth factor-DD
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Score 604; DB 7; Length 126; Pred. No. 1.4e-47; Mismatches 8; Indels

3;

Query Match
Best Local Similarity 91.3%;
Matches 115; Conservative

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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
                                                                                   61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYGMDVWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for stading various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
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                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMVPNSGNTGY
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                      Anti-human PDGF-D antibody protein related sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 202; 255pp; English
                                                                                                                                                                                                                                                      ADK18778 standard; protein; 126 AA.
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Best Local Similarity 88.9
Matches 112, Conservative
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TVTVSS 126
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120 

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Search completed: April 25, 2007, 04:05:21 Job time : 109.271 secs
121 TVTVSS 126
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GenCore version 6.2.1
(c) 1993 - 2007 Biocceleration Ltd.
                        Copyright
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 04:05:37 ; Search time 10 Seconds (without alignments) 1261.509 Million cell updates/sec

US-10-665-383-22 666

QVQLVQSGAEVKKPGASVKV........VIVHYGMDVWGQGTTVTVSS 126 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 80:\* Database :

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq heavy chain V r	Ig heavy chain V r		heavy	heavy	Iq heavy chain V r	heavy	heav	i-Sm antibody	heav	Ig heavy chain V r	b	ים	g heavy	g heavy	g heavy	g heavy	heavy	Ig heavy chain V r	מי	g heavy chain	g heavy	י ט	heavy cha	ь	heavy chain V	g heavy	Ig heavy chain V r	
SUMMARIES	Đ.	S34014	160	31	639	2691	7	S36265	248	849530	D33548	836260	\$23623	PH1666	S19665	PH0961	S26792	PH0955	S36271	PH0954	PH0960	B33548	C33548	S14683	S26938	PH1667	S31680	ı۸	PH0958	
	DB	7	7	~	~	7	0	7	0	7	7	Ŋ	0	0	~	0	0	N	7	7	0	7	7	0	N	0	0	7	0	•
	Length	127	136	132	129	98	110	118	142	135	123	129	171	118	124	119	131	127	122	132	136	126	133	627	96	114	117	117	122	•
æ	Query Match	85.5	83.3	79.6	78.0	77.6	77.0	76.9	75.8	75.4	74.4	74.1			73.0			70.2	70.0	70.0	70.0	8.69	69.4	69.4	69.2	69.2	69.2	69.2	69.2	
	Score	569.5	555	530	519.5	517	513	512	504.5	. 502	495.5	493.5	492	486	486	475.5	473.5	467.5	466.5	466	466	465	462.5	462.5	461	461	461	461	461	
	Result No.	7	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	ć

Ig heavy chain V r	i-PR2	Ig heavy chain V r	heavy	Ig heavy chain V r	heavy	Ig heavy chain V r	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	Ig heavy chain V r
144151	PL0105	PH1669	PH1668	S26912	869899	S20783	S68170	EIHUND	PH0957	A33548	PH0962	S19245	S26789	826920	PH0952
7	7	~	N	N	N	~	N	ч	~	~	~	~	~	~	~
126	160	110	109	86	104	121	125	143	125	129	120	142	120	96	128
0.69	68.7	68.5	68.1	68.0	67.8	67.8	67.8	67.7	67.5	67.5	67.4	67.3	67.0	66.4	66.4
	457.5 68.7	456 68.5		453 68.0		451.5 67.8				449.5 67.5				442 66.4	

## ALIGNMENTS

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R;Mariette, X.; Tsapis, A.; Brouet, J.C.

Bur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A;Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIV----HYGMDVW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFKGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARALSI---GVAVIRGYYYALDVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQMVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPSSGNTGY 60
Ig heavy chain V region - human
C'Species: Homo sapisens (man)
C'Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C'Accession: S34014; S30535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 127;
                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000176D31; EMBL:Z18321
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;Is-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 569.5; DB 2
Pred. No. 3.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
85.5%; Score 569.5;
Best Local Similarity 85.4%; Pred. No. 3.8e
Matches 111; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 GQGTTVTVSS 126
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GQGTTVSVSS 127
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Best Local Similarity
                                                                                                                                                                                                   A, Accession: S34014
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-127 < MAR>
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999
C;Accession: 831600
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-136 <CUI> A;Cross-references: UNIPARC:UP10000116453; EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology

Gaps

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A; Molecule type: DNA
A; Residues: 1-98 < TOMS.
A; Cross-references: UNIPARC:UP10000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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A,Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A,Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
                                                                                                                                                                                                                                              61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITF---GGVIVHYGMDVWG 117
                                                                                                                                                                                                                                                                        C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWYRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
                                                Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 85.6%; Pred. No. 3.8e-39; Similarity 85.6%; Pred. No. 3.8e-39; Si. Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (clone 2A12) - human (fragment)
                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 517; DB 2; I
Pred. No. 1.5e-39;
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                                              78.0%; Score 519.5; DB 2 ilarity 79.1%; Pred. No. 1.2e-39; Conservative 8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (DP-15) - human (fragment)
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100.0%; Pred. No....
0; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
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Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                   118 QGTTVTVSS 126
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                                                Query Match
Best Local Similarity
Matches 102; Conserv
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Best Local Simi
Matches 101;
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A;Residues: 1-132 <CUI>
A;Residues: 1-132 <CUI>
A;Cross-references: UNIPARC:UPI0000116454; EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831596
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Accession: $31596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                β
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A;Residues: 1-129 <FIG>
A;Cross-references: UNIPARC:UP1000011663A; EMBL:Z31680; NID:g509786; PIDN:CAA83485.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                             61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                             20 QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                          Length 136;
                                                                                                                           Indels
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                                                                          Score 555; DB 2;
Pred. No. 8.1e-43;
                                                                          Query Match
83.3%; Score 555; DB
Best Local Similarity 85.7%; Pred. No. 8.1e
Matches 108; Conservative 2; Mismatches
  C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                               TVTVSS 126
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A;Cross-references: UNIPARC:UP100001166FF; EMBL:246348; NID:9560839; PIDN:CAA86467.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
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                                                                                                                                                                                                                                                                                                                                      C;Accession: S49530 C;Accession: S49530 C;Accession: Salt, D;Accession: S49530 C;Accession: Submitted to the RMBL Data Library, October 1994 A;Description: Molecular characterization of natural human anti-Sm autoantibodies. A;Reference number: S48797
                           AQKFQGRVTMTRNTSISTAYMBLSSLRSEDTAVYYCARD-VMITFGGVIVHYGMDVWGQG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 502; DB 2; Length 13
Pred. No. 4.5e-38;
6; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                       anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.6e-37;
3; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.48;
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Best Local Similarity 77.8
Matches 98; Conservative
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                                                                                               TTVTVSS 126
                                                                                                                                  TLVTVSS 137
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
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A32483

1g heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
Filarrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, G Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human. hybridoma cells usi
                                                                                                                                                                                                                                                      S36265

19 heavy chain V region (clone alpha-MUCl-1) - human (fragment)

(5)Species: Homo sapiens (man)

(5)Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

(5)Accession: 836265

(6)Accession: 836265

(7) R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

(8) R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

(8) R;Griffiths, A.D.; Mullipodies with high specificity from phage display libraries.

(8) R;Greence number: 836265

(8) R;Catus; preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AOKFOGRVIMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
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78.6%; Pred. No. 5e-39;
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A; Residues: 1-118 <GRI>
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-142 <LAR>
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C,Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
Bxp. Med. 179, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo.
A;Reference number: PH1642; MUID:93301610; PMID:8315388
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C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: 81966; S24442
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, A, Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
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A;Residues: 1-40, GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
A;Residues: 1-40, GLSGWDGSALTMVTQSILDK',51-118,'T',120-124 
A;Cross-references: UNIPARC:UP10000115FE6; EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID
A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the s'
C;Superfamily: immunogloblin V region; immunoglobulin homology
C;Reywords: hererotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
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C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heteroteramer; immunoglobulin
F, 7-90/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-124 <MAR>
A;Cross-references: UNIPARC:UPI0000176B80; EMBL:X61647
                                                                                                                                                                                                                                 (g heavy chain V region (clone 6C9) - human (fragment)
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Pred. No. 1.1e-36;
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ilarity 79.3%;
Conservative
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                                                                                      140 MVTVSS 145
                             121 TVTVSS 126
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Best Local Similarity
Matches 96; Conserv
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nes 95; Conserv
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A;Molecule type: mRNA
A;Residues: 1-118 <HIL>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: 823623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Reference number: 823623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                    C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J EMbJ J. 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPARC:UPI0000118DEB; EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                               ,Species: Homo sapiens (man)
,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                               Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
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Pred. No. 2.5e-37; ....matches 15; Indels
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118 VWGKGTTVTVSS 129
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Best Local Similarity
                                                           121 TVTVSS 126
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Matches 94; Conserv
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A; Residues: 1-171 <OLE>
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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PH0961
[19 heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-119 < MAR.
A; Cross-references: UNIPARC:UPI000176CE5
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: complementarity-determining 3
F;99-107/Region: complementarity-determining 3
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Search completed: April 25, 2007, 04:06:40 Job time : 9.61017 secs

TVTVSS 126 |||||| TVTVSS 119

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RESULT 2
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ID Q9UL95_HUMAN
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Matches
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Q6n030
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Q6wy24
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Q9brv0
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Q94km15
Q954q9
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Q95k05
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Q9u195
GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OBWY24_HUMAN
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HVIC_HUMAN
O9GYZ2_MOUSE
O9BROW HUMAN
HV1B_HUMAN
HV1G_HUMAN
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Q6N09S HUMAN
QSBJZ2 RAT
Q6P089 HUMAN
QSEBMZ HUMAN
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Q9UL94 HUMAN
Q9UL92 HUMAN
Q6N030 HUMAN
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Q924Q9_MOUSE
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091WT1 - MOUSE
HV03 MÖUSE
094298 - HUMAN
092406 - MOUSE
065ZR6 - MOUSE
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Listing first 45 summaries
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Q924q3 mus musculu Ofrif1 homo garien	Q92583 mus musculu	Q924q4 mus musculu	Q924r1 mus musculu	P01757 mus musculu	Q6zp87 homo sapien	Q991c4 mus musculu	Q4qqw0 rattus norv	Q8vcx7 mus musculu	P01756 mus musculu	Q6nsa4 homo sapien	Q924r4 mus musculu
Q924Q3_MOUSE	Q925S3_MOUSE	Q924Q4_MOUSE	Q924R1 MOUSE	HV13 MOUSE	Q6ZP87 HUMAN	Q99LC4 MOUSE	O4OOWO RAT	Q8VCX7 MOUSE	HV12 MOUSE	Q6NSA4 HUMAN	Q924R4_MOUSE
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146	147	141	145	117	208	463	591	613	117	120	145
60.3	60.1	60.1	59.0	59.8	59.8	59.8	59.8	59.8	59.7	59.5	59.5
401.5	400.5	400	399	398.5	398.5	398	398	398	397.5	396	396
32	34	32	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVI-----VHYGMDVW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLVQSGAEVKKRGASVKVSCKASGYTFSNYYMMVRQAPGQAPEMMGVINPSGGSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.6%; Score 517; DB 2; Length 159; larity 75.4%; Pred. No. 2.2e-45; Conservative 16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Tilson M.D.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRR07110; Ig-like.
InterPro; IRR07110; Ig-like.
InterPro; IRR013106; Ig_wb.
InterPro; IRR013106; Ig_V-set.
InterPro; IRR013106; Ig_V-set.
SMART; SM00409; IG; I.
SMART; SM00409; IG; I.
SMART; PSS0835; IG_IKE; I.
Immunoglobulin domain.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
Q96QSO HUMAN PRELIMINARY; PRT; 159 AA. 096QSO; 01-DEC-2001, integrated into UniprotKB/TrEMBL. 01-DEC-2001, sequence version 1. 18-APR-2006, entry version 21. Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY039025; AAK82649.1; -; mRNA.
HSSP; P01869; 1AE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 GQGTTVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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Les 98, Conserv
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PRT; PRELIMINARY;

125 AA.

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Q9UL94 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                   01-MAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                              NUCLEOTIDE SEQUENCE.
MEDILINE-982771139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629; Kontermann R.E., Wing M.G., Winter G.;
                                                                                                                                                                                                                                                                                                                                                                                                Score 495.5; DB 2; Length
Pred. No. 2.9e-43;
9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                  125 125
125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998)
          01-MAY-2000, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 AA.
                                                                                                                                                                                                                               EMBL; AF035019; AAD56255.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QG5ZC8 HUMAN PRELIMINARY; PRT;
Q65ZC8;
                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR013599; Ig-sub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR03596; Ig-V-set_sub.
Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-0CT-2004, sequence version 1.
18-APR-2006, entry version 10.
                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 74.48;
76.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 76.6
nes 98; Conservative
                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTMVTVSS 125
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                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                         HSSP; P01751; INQB. SMR; Q9UL95; 1-122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=scFv;
                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
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                                                                                                                                                                     Eetus."
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18.APR-2006, entry version 2.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleos
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match. 73.3%; Score 488.5; DB 2; Length Best Local Similarity 74.6%; Pred. No. 3.3e-42; Matches 94; Conservative 14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26127 MW; 4B1F17868338F2BF CRC64;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
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                                                                                                                                                                   EMBL, Y13057; CAA73500.1; -; mRNA.
InterPro; IPR00510; Ig-like.
InterPro; IPR00599; Ig-gub.
InterPro; IPR003599; Ig-gub.
InterPro; IPR003596; Ig-V-set_sub.
Pfam; PF07686; V-set_2.
SWART; SM00409; IG; 2.
SWART; SM00406; IGv, 2.
PROSITE; PS50835; IG_LIKE; 2.
Immunoglobulin domain.
NON TER 1
NON TER 244 244
SEQUENCE 244 AA; 26127 MW; 4BIF1
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InterPro; IPR007110; Ig-like.
InterPro; IPR013199; Ig-gub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR003596; Ig-V-set_sub.
Pfam; PR07686; V-set; 1.
SWART; SM00409; IG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Rectum tumor;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
NUCLEOTIDE SEQUENCE.
                                        TVTVSS 126
                                                                               119 LVTVSS 124
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LinkHub; Q6N030; -.
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                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                               QEN030 HUMAN
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92;
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                                                                                                                                                                                                                                                                                  AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEMMGIINPSGGSTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                    1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                           7;
                                                                                                    DB 2; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleosi
Mammalia; Butheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 124;
                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                             13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                72.1%; Score 480.5; DB 75.4%; Pred. No. 1e-41; ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 479;
Pred. No. 1
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InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-aub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR03596; Ig-V-set_sub.
Pfam; PF07686; V-set; 1.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UL92 HUMAN PRELIMINARY;
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Immunoglobulin domain.

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NON TER 119 119
SEQUENCE 119 AA; 13
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                                                                                                Query Match
Best Local Similarity
Matches 95; Conserv
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61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSRF--DYWGQGT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Beta.2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0010803; P:MHC class I receptor activity; IEA.

R GO; GO:0019885; P:antigen presentation, endogenous antigen; IEA.

R GO; GO:0019885; P:antigen presentation, endogenous antigen; IEA.

R InterPro; IPR001005; HTHARAC.

R InterPro; IPR001005; HTHARAC.

R InterPro; IPR001006; Ig-MHC.

R InterPro; IPR001006; Ig-WHC.

R InterPro; IPR001006; Ig-WHC.

R InterPro; IPR001006; Ig-W-set_sub.

R Pfam; PF07654; CI-set; 3.

R Pfam; PF07654; CI-set; 1.

SWART; SM00409; IG; 1.

R SMART; SM00406; IGv. 1.
                                                                                                                                                                                                                                                                                                                                                                                             05-UU-2004, integrated into UniProtKB/TrEMBL.
05-UU-2004, sequence version 1.
27-UUN-2006, entry version 19.
27-UUN-2006, entry version 19.
Name-DKFZp686I15212,
Name-DKFZp686I15212,
Bumo applient (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
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PROSITE; PS000835; IG TKE; 4.
PROSITE; PS00290; IG THE; 4.
PROSITE; PS00290; IG THE; Hypochetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 518;
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                                                                                                                                                                                                                                                                                                                                 518 AA.
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No. 10 (2010) 16021; Clintegral to membrane; IEA.

No. GO; GO:0016021; Clintegral to membrane; IEA.

No. GO; GO:0016020; Clemenbrane; IEA.

No. GO; GO:0016020; Clemenbrane; IEA.

No. GO; GO:0019881; P:antigen processing, endogenous antigen; IEA.

No. GO; GO:0019885; P:antigen processing, endogenous antigen; IEA.

No. GO; GO:0019885; P:antigen processing, endogenous antigen; IEA.

No. InterPro; IPR00359; Ig_Cl.set.

No. InterPro; IPR00359; Ig_Cl.set.

No. InterPro; IPR00359; Ig_W.set.

No. INTERPRO; IG_W.set.

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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                     Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
                                                                                     Homo sāpiens (Human).
Bukaryota, Metazooa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Hypothetical protein DKFZp686C02220 (Fragment)
Name=DKFZp686C02220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF283666; AAL36987.1; -; mRNA.
HSSP; P01876; 10W0.
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27-JUN-2006, entry version 25
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Q6N091;
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nes 90; Conservative
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TLVTVSS 144
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                                               SNC66 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AOKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG---GVIVHYGMDVWG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Human rectum tumor;
The German Human cDNA Consortium;
Pousta A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Wail B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01751; 1A6W.

SMR; Q6N041; 268-476.

InterPro; IPR003591; Ig_c1:set.

InterPro; IPR003599; Ig_c1:set.

InterPro; IPR003599; Ig_whc.

InterPro; IPR013106; Ig_whc.

InterPro; IPR013106; Ig_whc.

InterPro; IPR013106; Ig_v-set.

InterPro; IPR003596; Ig_v-set.

InterPro; IPR003596; Ig_v-set.

InterPro; IPR003596; Ig_v-set.

InterPro; IPR003596; Ig_w-set.

InterPro; IPR003596; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, sequence version 1.
18-APR-2006, entry version 13.
Hypotherical protein DKFZp686016217 (Fragment)
Name-DKFZp686016217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBWY24_HUMAN PRELIMINARY; PRT; 497 AA. 08WY24; 01MAR-2.2002, integrated into UniProtKB/TrEMBL. 01-MAR-2002, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                         498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BX640710; CAE45829.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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    121 TVTVSS 126
                                                                                          136 LVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         Q6N041_HUMAN
Q6N041;
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Marcel Dekker, New York (1978).
-!- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                         38 QVQLVQSGAEVKKPGASVKVSCKASGYTFSDHSITWLRQAPGQGLEWIGWISAYSGQTYY 97
                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                               Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 20-147.

Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; (In) Bach M.K. (eds.);
                                                                                                                                                                                                                                                                                                                                     500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;
                                                                                                                                                                                                                                                   SWART; SM00409; IG; 1.
SWART; SM00409; IG; 1.
SWART; SW00407; IGZ; 2.
SWART; SW00406; IGY; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG MHC; UNIXOWN 2.
Hypothetical protein; Immunoglobulin domain; Repeat.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2006, entry version 47.
Ig heavy chain V-I region ND precursor (Fragments).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVIC HUMAN STANDARD; FAA., POLT44; 21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 01-DEC-2000, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                           67.8%; Score 451.5; DB 2
70.6%; Pred. No. 5.2e-38;
tive 11; Mismatches 23
                                                                                                                            HSSP, PO1751; 1A6W.
SMR; Q6N031; 270-478.
InterPro; IPR007110; Ig-like.
InterPro; IPR0071006; Ig_MHC.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003599; Ig_wub.
InterPro; IPR03599; Ig_v-set.
InterPro; IPR03596; Ig_v-set.
InterPro; IPR03596; Ig_v-set.
InterPro; IPR03596; Ig_v-set.
                                                                                                                      EMBL; BX640625; CAE45779.1; -; mRNA.
           SSUE=Human rectum tumor;
le German Human cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83065234; PubMed=6815656;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                            Pfam; PF07654; C1-set; 2
Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
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Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001, sequence version 1.
18-APR-2006, entry version 22.
Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy chain variable region (Fragment).
Mus musculus (Mouse).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                GO: GO:0005576; C:extracellular region; NAS.
GO: GO:0003823; F:antigen binding; NAS.
GO: GO:0003823; F:antigen binding; NAS.
GO: GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V-set_sub.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 451; DB 1; Length 147;
Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song X.T., Feng Z.Q., Guan X.H.; Mamplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma japonicum."; Schistosoma japonicum."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V-I region ND/Frid=PRO_000015246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T -> V (in Ref. 2).
IH -> HI (in Ref. 2).
VG -> GV (in Ref. 2).
Missing (in Ref. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%; Prec. ...
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Q9GYZ2;
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hes 86; Conservative
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                                                                                                                               HSSP; P01751; 1NQB.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                         NIH MGC Project
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HV1B HUMAN
ID HV1B HUMAN
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Mammalian Gene Collection Program Team,

Rausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Bueter E., Shemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Bueter K.H., Schaefer C.F., Bhat N.K.,

Aptichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

And M., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR---DVMITFGGVIVHYGMDVWG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                        66.3%; Score 441.5; DB 2; Length 119; 67.4%; Pred. No. 1.1e-37; tive 13; Mismatches 16; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                             119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001, integrated into UniProtKB/TrEMBL.
01-JUN-2001, sequence version 1.
25-JUL-2006, entry version 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Prostate;
PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 AA
                                                                                       SMR; Q9GYZZ; 1-119.
InterPro; IPR007110; Ig-like.
InterPro; IPR003199; Ig-gub.
InterPro; IPR013106; Ig V. set.
InterPro; IPR003596; Ig_V-set_gub.
Pfam; PF07686; V-set; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
                                             EMBL; AF282622; AAG01452.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBRVO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              | Similarity 67.49
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OGTTVTVSS 119
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                                                                                                                                                                                                                                                                                                         Immunoglobulin domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                      P01751; 1A6W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGHAl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=IGHA1;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 3
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      090 BRV0

      090 BRV0

      090 BRV0

      091 BDT

      090 BDT

      091 BDT

      092 SDT

      093 BDT

      094 BDT

      095 BDT

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61 AQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDV--MITFGGVIVHYGMDVWGQ 118
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                                                                                                                                                                                                                                                                               HSSP; PO1876; 10M0.

SMR; Q9BRV0; 25-300, 270-478.

Ensembl; ENSGG0000130076; Homo sapiens.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                          Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP00047; ig; 1.
Pfam; PP07686; V-set; 1.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
SMART; SM002200; IG HIC; UNKNOWN 1.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986, integrated into UniProtKB/Swiss-Prot... 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 43. Ig heavy chain V-I region HG3 precursor.
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR013151; IG.
InterPro; IPR0013151; IG.
InterPro; IPR003501; IG-11ke.
InterPro; IPR003506; IG_NHC.
InterPro; IPR003599; IG_sub.
InterPro; IPR013106; IG_V-set.
InterPro; IPR013106; IG_V-set.
InterPro; IPR013506; IG_V-set.
PROM5596; IG_V-set.
PROM5596; IG_V-set.
                                                                                                                                                                                                                                                        EMBL; BC005951; AAH05951.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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140 GTTVTVSS 147
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NUCLEOTIDE SEQUENCE.
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us-10-665-383-22.rup

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01-OCT-2003, sequence version 1. 27-JUN-2006, entry version 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q727P5 HUMAN
ID Q727P5_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                          >117
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                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGHG1 protein.
Name=IGHG1;
                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                     Best Local
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                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    four human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ur. J. Immunol. 23.846-851(1993).
!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=33209281; PubMed=7681398;
Mariette X., Tsaplis A., Brouet J.C.;
"Nuclectidic sequence analysis of the variable domains of four
monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                           Length 117;
                                                                                                                                                                                                                                                    Ig heavy chain V-I region HG3./FTid=PRO_000015244.
                                                                                                                                                                                                                                                                                                                          Score 437; DB 1; Length 11
Pred. No. 3.2e-37;
6; Mismatches 8; Indels
                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                          20 >117 Ig-11xe.
117 117
117 AA; 12946 MW; 2D3F92FCGOCDIFE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
                                                                                                                 GO; GO:0005576; C:extracellular region; NAS. GO; GO:000382; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR07110; IG-like.
InterPro; IPR07110; IG-like.
InterPro; IPR03596; IG_V-set_sub. Ffam; PF07686; V-set_i. ISWART; SM04406; IG_V: I.
SWART; SM04406; IG_V: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991, sequence version 1.
30-MAY-2006, entry version 38.
Ig heavy chain V-I region V35 precursor.
Homo sapiens (Human).
                                                         EMBL; J00240; AAA52988.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                          65.6%;
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                              HSSP; P01751; 1NQB.
SMR; P01743; 20-117.
LinkHub; P01743; -.
                                                                       PIR; A02024; HVHUHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy-chain locus.
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NON TER
SEQUENCE
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HV1G HUMAN
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A Carausberg R.L., Feingold E.A., Orouse L.H., Derge J.G.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhar N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rheby J., Helton E., Ketteman M., Maddan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerthield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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Mammalia; Butheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                GO; GO: 0003825; C: extracellular region; NAS.
GO; GO: 0003825; P: antigen binding; NAS.
R GO; GO: 0006955; P: immune response; NAS.
R InterPro; IPR00110; Ig-like.
InterPro; IPR0013106; Ig-V-set.
R InterPro; IPR001356; Ig-V-set.
R InterPro; IPR001556; Ig-V-set.
R InterPro; IPR00156; Ig-V-set.
R InterPro; IPR00156; Ig-V-set.
R InterPro; IPR00156; Ig-V-set.
R InterPro; IPR00116; IG-V-set.
R InterPro; IPR00116; IG-V-set.
R InterPro; IPR00116; IG-V-set.
R InterPro; IPR00116; IG-V-set.
R INTERPROSE R IN
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EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA PIR; S00476; HVHU35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 437; DB 1;
Pred. No. 3.2e-37;
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85.7%; Pred. No. 3.-
5; Mismatches
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                                                                                                                               HSSP, P01751; INQB.
SMR; P33083; 20-117.
Ensembl; RNSG0000130076; Homo sapiens.
LinkHub; P23083;
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61 AQKFQCRVTMTRNTSISTAYMELSSIRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                              NIH MGC Project;
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.4%; Score 429; DB 2; Length 469; Best Local Similarity 65.9%; Pred. No. 1.1e-35; Matches 83; Conservative 15; Mismatches 22; Indels
                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC051328; AAH51328.1; -; mRNA.
HSSP; P01857; 1HZH.
SMR; Q7Z7P5; 20-469.
                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                               TISSUE=Spleen;
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Search completed: April 25, 2007, 04:06:37 Job time : 86.7797 secs

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Scoring table:

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Score 526; DB 2; Length 120;
Pred. No. 5.5e-45;
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SOFTWARE: PERCENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-A06-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REJERRENGE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTR: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09025769B

Patent No. 630064

GENERAL INFORMATION:
APPLICANT: Fack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
ITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
US-08-561-521-10
PCT-US95-01219-10
US-08-202-047-22
US-08-38-954-41
US-08-438-954-41
US-08-453-164A-19
US-08-613-024-18
US-08-452-164A-19
US-08-450-164A-19
US-08-310-386A-65
US-08-310-386A-65
US-08-310-386A-65
US-08-311-645-65
US-08-931-645-65
US-08-931-645-65
US-08-931-645-65
US-08-931-645-65
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US-08-487-113D-86
US-08-473-503-86
                                                                                                                                                                                                                                                                                                                     US-08-964-690-23
US-08-482-882-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.0%;
83.3%;
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
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Best Local Similarity
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      559, Appl
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696.311 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/HCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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                                                                                                                                                              April 25, 2007, 04:06:51 ; Search time 16 Seconds
                             6.2.1
Biocceleration Ltd
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US-09-025-769B-59

US-09-490-070A-36

US-09-490-153-59

US-09-490-153-59

US-09-490-153-59

US-09-490-324-36

US-09-025-769B-22

US-09-025-769B-22

US-09-025-769B-22

US-09-05-033-4-59

US-09-490-133-22

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US-09-490-133-22

US-09-490-133-22

US-09-490-133-22

US-09-490-133-22

US-09-45-809A-96

US-09-515-697-96

US-01-310-613A-21

US-08-515-697-94

US-08-477-281A-94

US-08-477-281A-94

US-08-472-281A-94

US-08-472-281A-94

US-09-462-1400-105

US-09-199-149-3

US-08-525-539A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                              650591 seqs, 87530628 residues
                             version (
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                             GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                  US-10-665-383-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
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LENGTH: 120 amino acids
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STRANDEDNESS: <Unknown>
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
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Matches 105; Conservative
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121 TVTVSS 126
                                            115 LVTVSS 120
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US-09-490-070A-59
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                                       셤
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                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWYRQAPGQGLEMMGWINPNSGGTNY 60
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                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
6; Gaps
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COMPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: FC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRICH APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., ESQ.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 526; DB
Pred. No. 5.5e-
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09025769B Patent No. 6300064
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Best Local Similarity 83.3%;
Matches 105; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-09-025-769B-59
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                                                                                                                                                                                                                        121 TVTVSS 126
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10021
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
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                                                                APPLICANT: Knappik, Achim
Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 526; DB 2;
Pred. No. 5.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-070A-36
Sequence 36, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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Plueckthun, Andreas
                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                    ZIF: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 526; DB 2; Length 120;
Pred. No. 5.5e-45;
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                                                                                                                                           Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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MOLECULE TYPE: protein
US-09-490-070A-59
Sequence 59, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
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Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 120 amino acids TYPE: amino acid
                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
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Moroney, Simon
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: USA
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vid.
Ca, Lining
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 120;
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Pred. No. 5.5e-45;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-490-153-59
; Sequence 59, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                           STATE: New York
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PRIOR APPLICATION DATA:
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                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 526; DB 2;
Pred. No. 5.5e-45;
5; Mismatches 10
                                                                                                                                               CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-5an-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.0%;
Best Local Similarity 83.3%;
Matches 105; Conservative S
                                ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STATE: New York
COUNTRY: USA
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQXEQGRUTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT
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APPLICANT: Roappik, Achim
Back, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCE: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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APPLICATION NUMBER: US/09/490,324
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
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Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels
                                                                             FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., ESG. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
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Query Match 78.8%; Score 524.5; DB 2; Best Local Similarity 81.7%; Pred. No. 7.5e-45; Matches 103; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
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TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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Pack, Peter
Ilag, Vic
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  TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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                                                                                    LENGTH: 117 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   MOLECULE TYPE: protein US-09-025-769B-22
                                                                                                                                                  linear
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                                                                                                                                                  TOPOLOGY:
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COMPUTE TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99025,769B
FILING DATE: 18-FEB-1998
PRICA PROBA PPLICATION NUMBER: EP 95 11-3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESG.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 526; DB 2; Length 120
Pred. No. 5.5e-45;
5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 1lag, Vic
APPLICANT: Ge, Liming
APPLICANT: Grone, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/ACENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.0%;
Best Local Similarity 83.3%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 LVTVSS 120
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                 Gaps
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COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

COMPATION:

APPLICATION CANALY OF PERFORMED AND PERFORMED A
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DB 2; Length 117;
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYXCARD------GDGGFDYWGQGT 111
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                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
                                                                                                                                       61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT
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                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
           Gaps
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           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
           9; Indels
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Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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81.7%; Pred. No. 7.5e-45;
iive 5; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/025,769
FILLING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-AUG-1995
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MORPHO/5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: James F. Haley, Jr., REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 117 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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Best Local Similarity 81.77
Matches 103; Conservative
           Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                121 TVTVSS 126
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                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTWTRDTSISTAYWELSSLRSDDTAVYYCARD------GDGGFDYWGQGT 111
                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                            Gaps
                                                                                                                                            9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.8%; Score 524.5; DB 2; Length 117; 81.7%; Pred. No. 7.5e-45;
                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                   DB 2;
                                                                                                 Score 524.5; DB 2
Pred. No. 7.5e-45;
5; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FBB-1998 APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/490,153
FLIING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-070A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
                                                                                                 78.8%;
81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                               Query Match
Best Local Similarity 81.7°
Matches 103; Conservative
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STATE: New York
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Best Local Similarity
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US-09-490-153-22
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61 AQKFQGRVTWTRNTSISTAYMBLSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
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                                        61 AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.6%; Score 517; DB 2; I Best Local Similarity 100.0%; Pred. No. 4.2e-44; Matches 98; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDLUM TYPR: Diskette
COMPUTER: Diskette
APPLICATION NUMBER: DISKETE
APPLICATION NUMBER: DISKETE
COMPUTER: 
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                                                                                                                                                                                                                                                                                                                                                                                         US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Zetent No. 6096878
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
Matsuda, Fumihiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 117 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                    121 TVTVSS 126
                                                                                                                                                                                                                            112 LVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRECT: 220
STREET: 220
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US-09-515-697-96
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Sequence 28, Application US/09859053
Sequence 28, Application US/09859053
Fatent No. 6803039
GENERAL INFORMATION:
APPLICANT: Texui, Taxashi
APPLICANT: Texui, No. 6803039uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
FILLE OF INVENTION: PARRAMCEUTICAL USE THEREOF
FILLE OF INVENTION: UMBER: US/09/859,053
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: JP 2001-99508
FRIOR APPLICATION NUMBER: JP 2001-03-30
FRIOR FILLING DATE: 2001-03-30
FRIOR FILLING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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COMPUTE: US

COMPUTE: US

COMPUTE: Diskette

COMPUTE: Diskette

COMPUTE: IBM Compatible

COMPUTE: IBM Compatible

COMPUTE: SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/515,697

FILING DATE: 29-Feb-2000

FRIOR APPLICATION NUMBER: US/08/545,809

FILING DATE: 27-MAR-1996

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AOXFOGRUTMTRNTSISTAYMELSSLRSEDTAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.6%; Score 517; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.2e-44;
Matches 98; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                             ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 117 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
                                                                  NUMBER OF SEQUENCES: 145
                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-859-053-28
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; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match
Best Local Similarity 78.6%; Pred. No. 1.1e-42;
Matches 99; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

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1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNNPNSGNTGY 60

DD 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYWHWVRQATGQGLEWMGWNNPNSGNTGY 79

OY | 1QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYWHWVRQAPGQGLEWMGWNNPNSGNTGY 79

OY | 61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVWTFGGVIVHYGMDVWGGT 120

OY | 121 TVTVSS 126

Db | 139 MVTVSS 144

Search completed: April 25, 2007, 04:08:32
JOb time: 15.839 secs
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April 25, 2007, 04:18:18 ; Search time 47 Seconds (without alignments) 1251.741 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKV......VIVHYGMDVWGQGTTVTVSS 126
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Sequence
Sequence
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Sequence
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-10-041-860-199

US-10-041-860-236

US-10-041-860-236

US-10-041-860-204

US-10-041-860-204

US-10-041-860-204

US-10-041-860-204

US-10-041-860-201

US-10-041-860-19

US-10-041-860-19

US-10-041-860-201

US-10-041-860-202

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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	ALIGNMENTS					
Sequence 47, Appl	US-10-982-440-47	S	120	81.7	544	45
Sequence 47, Appl	US-10-269-805-47	4	120	81.7	544	44
Sequence 93, Appl	US-11-090-847-93	9	242	81.9	545.5	43
Sequence 919, App	US-11-266-444-919	9	249	82.4	549	42
	US-11-054-515-919	9	249	82.4	549	41
Sequence 919, App	US-10-293-418-919	4	249	82.4	549	40
Sequence 919, App	US-09-880-748-919	m	249	82.4	549	39
Sequence 3, Appli	US-10-290-703-3	4	476	84.8	564.5	38
Sequence 3, Appli	US-09-747-669-3	٣	476	84.8	564.5	37
Sequence 2, Appli	US-10-665-383-2	4	125	85.2	567.5	36
Sequence 372, App	US-10-041-860-372	4	125	85.2	567.5	35
_	US-10-041-860-237	4	125	85.2	567.5	34
	US-10-041-860-200	4	125	85.2	567.5	33
4	US-10-041-860-48	4	125	85.2	567.5	32
Sequence 66, Appl	US-10-665-383-66	4	127	87.2	580.5	31
-	US-10-041-860-360	4	127	87.2	580.5	30
Sequence 242, App	US-10-041-860-242	4	127	87.2	580.5	29
Sequence 205, App	US-10-041-860-205	4	127	87.2	580.5	28

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AQKFQGRVTMTRNTSISTAYMBLSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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  Sequence 21, Application US/10041860

Sequence 21, Application US/10041860

Publication No. US2030157109A1

GENERAL INFORMATION:

APPLICANT: Ocrvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Binyam

TITLE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX.05107041,860

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SORVIDANS: Fabrica for Windows Version 4.0
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100.0%; Score 666; DB 4;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0;
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US-10-041-860-21
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US-10-041-860-21
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Sequence 199, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi

Sequence

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TVTVSS 126
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              APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THRREOF
FILE REFERENCE: ABERNIX 05.1A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FREEEE/FOR WINDOWS Version 4.0
SEQ ID NO 199
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100.0%; Score 666; DB 4;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0;
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 126
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: homo sapiens
US-10-041-860-199
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; ORGANISM: homo sapiens
US-10-041-860-236
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PRESENT 4

1. Sequence 24, Application US/10041860

1. Sequence 25, Application US/10041860

1. Sequence 25, Application US/1065383

Matches 126; Conservation US/1065383

1. Sequence 27, Application US/1065383

Matches 27, Application US/1065383

MATCHES 21, Application US/1065383

MATCHES 21
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ORGANISM: homo sapiens
US-10-041-860-241
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TVTVSS 126
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Best Local Similarity
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                                                                                                       61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
                                                                                                                      61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMPNSGNTGY
                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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  Length 126;
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89.7%; Pred. No. 6.5e-50;
tive 6; Mismatches 7; Indels
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100.0%; Score 666; DB 4;
100.0%; Pred. No. 9.8e-56;
                           0; Mismatches
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
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Matches 113; Conservative
             Best Local Similarity 100.
Matches 126; Conservative
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ORGANISM: homo sapiens
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US-10-041-860-204
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LENGTH: 126
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                   90.8%; Score 605; DB 4; Length 126;
89.7%; Pred. No. 6.5e-50;
tive 6; Mismatches 7; IndelB
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 126
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen; Yang-Dong
APPLICANT: Chen; Yang-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binpand
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241
LENGTH: 126
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 113; Conservative
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CORGANISM: homo sapiens
US-10-041-860-204
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US-10-041-860-201
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APPLICANT: Floege, Juergen
APPLICANT: Reyt, Bruck
APPLICANT: LaRochelle, William
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WERTHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REPERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2003-09-16
PRIOR FILING DATE: 2003-09-16
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                                                                          APPLICANT: Correlan, Jose R.F.
APPLICANT: Correlan, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Prancine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bacabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
                                                                                                                                                                                                                                                                              FILE REPERENCE: ADGRANCY FILE REPERENCE: ADGRANCY CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER: OF SEQ ID NOS: 377 SOFTWARE: PastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 126
                      Sequence 349, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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Publication No. US20040141969A1
GENERAL INFORMATION:
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Best Local Similarity 89.7
Matches 113; Conservative
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CRCANISM: homo sapiens
US-10-041-860-349
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ORGANISM: homo sapiens
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Best Local Similarity
Matches 113; Conserv
        JS-10-041-860-349
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LENGTH: 126
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61 AQKEQGRUTIMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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1 OVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                           1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWANPNNGNTGY
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APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao-Dong
APPLICANT: Tang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: New APPLICANTON: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTIBORES
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: And Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Webzh, Binyam
TITLE OF INVENTION: THEREOF
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Pred. No. 8.1e-50;
3; Mismatches 8
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CURRENT APPLICATION NUMBER: US/10/041,860
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o. US20030157109A1
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.7%;
Best Local Similarity 91.3%;
Matches 115; Conservative
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TVTVSS 126
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; Publication No. US2030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao-Chi
; APPLICANT: Chen, Krancine
; APPLICANT: Chen, Krancine
; APPLICANT: Chen, Krancine
; APPLICANT: Beaabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES; TITLE OF INVENTION: ANTIBODIES
; 
                                                                                                                                                                                                                                                                                                                            Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.7%; Score 604; DB 4; Length 126; 91.3%; Pred. No. 8.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                        Score 604; DB 4;
Pred. No. 8.1e-50;
3; Mismatches 8;
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   CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SEQ ID NO 201
LENGTH: 126
2002-01-07
377
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.3%;
Matches 115; Conservative
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Best Local Similarity 91.3:
Matches 115; Conservative
                                                                                                                                                                                  TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-201
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ORGANISM: homo sapiens
US-10-041-860-288
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RESULT 14 US-10-665-383-18 Sequence 18, Application US/10665383 ; Publication No. US20040141969A1

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61 AQKFQGRVTMTRNTSISTAYMBLSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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Sequence 37, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Orovalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber, Richa
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APPLICANT: Keyt, Bruce
APPLICANT: LaRochelle, William
APPLICANT: LaRochelle, William
APPLICANT: Larochelle, William
TITLE CANT: Lichenstein, Henri
TITLE OF INVENTION: WETHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGR-DD ANTIBODIES
FILE REFERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/411,137
PRIOR PELING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SEQ ID NOS: 97
SEQ ID NO 18
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Pred. No. 1.9e-49;
6; Mismatches 8; Indels
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Best Local Similarity 88.9%;
Matches 112; Conservative 6
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US-10-041-860-37
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121 TVTVSS 126 |||||| 121 TVTVSS 126

Search completed: April 25, 2007, 04:22:51 Job time: 47.6271 Becs

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RESULT 2
US-11-109-181-199
; Sequence 199, Application US/11109181
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SOFTWARE: Fast
SEQ ID NO 21
LENGTH: 126
TYPE: PRT
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/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO7_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO1_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/USO1_NEW_PUB.pep:*
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Biocceleration Ltd
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US-11-109-181-199
US-11-109-181-236
US-11-109-181-204
US-11-109-181-204
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                  GenCore version (c) 1993 - 2007
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 QVOLVOSGAEVKKPG3
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seq length: 2000000000
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US-11-109-181-48

US-11-109-181-200

US-11-109-181-237

US-11-109-181-372

US-11-396-178-20

US-09-766-003-29

US-11-433-924-14

US-11-337-917-15

US-11-410-886-69

US-11-410-886-69

US-11-110-386-69

US-11-311-939-429

US-11-311-939-429

US-11-311-939-686

US-11-311-939-586

US-11-316-003-27

US-11-310-939-586

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### ALIGNMENTS

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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
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Sequence 21, Application US/11109181
| Publication No. US20060293506A1 |
| Publication No. US20060293506A1 |
| GENERAL INFORMATION: |
| APPLICANT: Corvalan, Jose R.F. |
| APPLICANT: Feng, Xiao-Chi |
| APPLICANT: Feng, Xiao-Chong |
| APPLICANT: Read, Kiao-Dong |
| APPLICANT: Gazit, Gadi |
| APPLICANT: Weber, Richard |
| APPLICANT: Weber, Sichard |
| PRIOR FILING DATE: 2005-04-18 |
| PRIOR APPLICATION NUMBER: US/10/041,860 |
| PRIOR FILING DATE: 2002-01-07 |
| NUMBER OF SEQ ID NOS: 377 |
| SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.8e-56;
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100.0%; Pre
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US-11-109-181-21
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 126;
                                GENERAL INCRAMINON:
GENERAL INCRAMINON:
GENERAL INCRAMINON:
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
GENERAL Fengine
APPLICANT: Peng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
FILE REPERENCE: AGGENIX.051A
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 126
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APPLICANT: Yang, Xiao-
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
APPLICANT: Weber, Richard
APPLICANT: ABGENIX: 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
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100.0%; Score 666; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 126
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Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
Publication No. US20060293506A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: homo sapiens
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US-11-109-181-236
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61 AQKFQGRVTMTRNTSISTAYMBLSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dng
APPLICANT: Tang, Xiao-Dng
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CHERN APPLICANTON: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE REPRENCE: ABGENIX. 051A
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/11/109,181
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 126
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100.0%; Pred. No. 1.8e-56;
tive 0; Mismatches 0;
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Publication No. US20060293506A1
GENERAL INPORMATTON:
APPLICANT: Corvalan, Jose R.F.;
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
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121 TVTVSS 126
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| Publication No. US20060293506A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Gradian Xiao-Chi
| APPLICANT: Feng, Xiao-Chi
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Gazt, Gadi
| APPLICANT: Rebach, Binyam
| APPLICANT: Mebar, Richard
| APPLICANT: Mebar, Binyam
| TITLE OF INVENTION: ATTIBEDDES
| TITLE OF INVENTION: THEREOF
| FILE REPERENCE: AGENIX.051A
| CURRENT APPLICATION NUMBER: US/11/109,181
| CURRENT FILING DATE: 2005-04-18
| PRIOR FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.8%; Score 605; DB 7; Length 126;
89.7%; Pred. No. 1.3e-50;
Live 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FESTESQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 126
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 126
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Best Local Similarity 89.7
Matches 113; Conservative
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Matches 113; Conservative
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-40
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVTVSS 126
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVTATDYYYGMDVWGQGT 120 0
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                                                                                                      APPLICANT: Orvelain, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Cazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bor INVERTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
FRIOR APPLICATION NUMBER: US/10/041,860
FRIOR FILING DATE: 2005-01-07
NUMBER OF SEQ ID NOS: 377
SEQ ID NOS: 377
SEQ ID NO 241
SEQ ID NO 241
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APPLICANT: Chen, Xiao-Dong
APPLICANT: Chen, Xiao-Dong
APPLICANT: Chen, Kanc-Dong
APPLICANT: Gait, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 126;
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Pred. No. 1.3e-50;
6; Mismatches 7;
US-11-109-181-241
; Sequence 241, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
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Publication No. US20060293506A1
GENERAL INFORMATION:
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Best Local Similarity 89.7%;
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homo sapiens
US-11-109-181-241
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61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 288
                APPLICANT: Chen, Francine APPLICANT: Chen, Francine APPLICANT: Gazit, Gadi APPLICANT: Weber, Richard APPLICANT: Weber, Richard APPLICANT: Weber, Richard APPLICANT: Weber, Barnyam TITLE OF INVENTION: ANTIBEDES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THERROF FILE REPRENCE: ABGENIX. 051A CURRENT APPLICATION NUMBER: US/11/109,181

CURRENT APPLICATION NUMBER: US/10/041,860

PRIOR APPLICATION NUMBER: 2005-04-18

NUMBER OF SEQ ID NOS: 377

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 201

LENGTH: 126
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Pred. No. 1.6e-50;
3; Mismatches 8; Indels
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Pred. No. 1.6e-50;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 288, Application US/11109181 Publication No. US20060293506A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.3%;
Matches 115; Conservative
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Best Local Similarity 91.3%;
Matches 115; Conservative
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Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: homo sapiens
US-11-109-181-201
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US-11-109-181-288
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                                                                                                                                                                                                                                                                                         61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGWDVWGQGT 120
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                                                                       Query Match 90.8%; Score 605; DB 7; Length 126; Best Local Similarity 89.7%; Pred. No. 1.3e-50; Matches 113; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Viao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Chan, Francine
APPLICANT: Chan, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
TITLE OF INVENTION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
FILE REPERENCE: ABGENIX.051A
CURRENT FILING DATE: 2005-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASELSEQ for Mindows Version 4.0
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; Sequence 201, Application US/11109181
; Enblication No. US20060293506A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     121 TVTVSS 126
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     ; OKGM11-109-181-349
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LENGTH: 126
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PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 202
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88.9%;
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Best Local Similarity 88.9
Matches 112; Conservative
                                                                                           TYPE: PRT
CRGANISM: homo sapiens
US-11-109-181-202
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US-11-109-181-239
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US-11-109-181-38
                                                                          LENGTH: 126
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AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVWGQGT 120
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                     61 AQKFQGRVTWTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                              APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Cazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVEXTION: THEREOF
FILE REFERENCE: ARCENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT PAPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2005-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corvalan, Jose R.F.
APPLICANT: Gradan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTHRODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.1%; Score 600; DB 7; Length 126; 88.9%; Pred. No. 3.8e-50; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 126
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                                                                                                                                                                                                     ; Sequence 37, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                            APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                 Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Gazit, Gadi
Weber, Richard
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Best Local Similarity 88.9
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: homo sapiens
US-11-109-181-37
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US-11-109-181-202
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APPLICANT:
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US-11-109-181-239

Sequence 239, Application US/11109181

Publication No. US20660293506A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Vang, Xiao-Chi

APPLICANT: Yang, Xiao-Dong

APPLICANT: Gazit, Gadi

APPLICANT: Rezabeh, Binyam

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION UNMBER: US/11/109,181

CURRENT FILING DATE: 2005-04-18

PRIOR FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 126

LENGTH: 126
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Query Match 90.1%; Score 600; DB 7; Length 12 Best Local Similarity 88.9%; Pred. No. 3.8e-50; Matches 112; Conservative 6; Mismatches 8; Indels
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Pred. No. 3.8e-50;
6; Mismatches 8
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us-10-665-383-24.rag

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	1	AUKIESSE AULT-IIUIIG	Adk18838 Anti-huma	Adk18837 Anti-huma	Adk18873 Anti-huma	-	Adl25414 Human mAb	Ads84414 Human ant	Adr68556 Anti-EPO-	Ads84470 Human ant	Adr68612 Human ant	Ads84402 Human ant	Adr68544 Anti-EPO-	Ads84452 Human ant	Adr68594 Human ant	Adk18841 Anti-huma	Aej60732 Sulfocore	Abg77160 Germline	Adr28582 Human ant	Aef54367 Human lig	Aef54346 Human lig	Aef34918 Human ger	Ael09667 Anti-IĞF1
SUMMARIES	ID		AUA.0330	ADK18838	ADK18837	ADK18873	ADK18803	ADL25414	ADS84414	ADR68556	ADS84470	ADR68612	ADS84402	ADR68544	ADS84452	ADR68594	ADK18841	AEJ60732	ABG77160	ADR28582	AEF54367	AEF54346	AEF34918	AEL09667
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de	Query Match	1000	2001	100.0	100.0	100.0	100.0	100.0	97.1	97.1	97.1	97.1	9.96	9.96	9.96	9.96	94.6	94.6	94.6	94.6	94.6	94.6	94.6	94.6
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AEL59900 ABG30494 ADS16571 ADC99789	ADD05393 ADF09831 ADK18842 ADK18916	ADK18892 ADK18612 ADK18602	ADK18810 ADK18844 ADK18808 ADK18807	ADK18604 ADP03996 ADL25422 ADL25426	ADL25442 ADO07289 ADP22368 ADP22401
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## ALIGNMENTS

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for stading various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention. Weber R; growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer. antiinflammatory; immunomodulator; cytostatic; gene therapy. Gazit G, Anti-human PDGF-D antibody light chain protein sequence. Chen F, Disclosure; SEQ ID NO 22; 255pp; English Yang X, ADK18598 standard; protein; 107 AA. Feng X, 06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860. 06-MAY-2004 (first entry) Corvalan JRF, Jia X, WPI; 2003-587119/55. (ABGE-) ABGENIX INC. WO2003057857-A2. 17-JUL-2003. Bezabeh B; 

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGP-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation,
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diseases, such as inflammation, autoimmunity and cancer.
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antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                    Anti-human PDGF-D antibody protein related sequence #63.
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Matches 107; Conservative
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Bezabeh B;
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                                                                                                                                                                                                                                        RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                          Length 107;
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                                                Score 558; DB 7; Pred. No. 2e-34;
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Matches 107; Conservative
                                                                                                Matches 107; Conservative
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                                                                                Local Similarity
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                        Sequence 107 AA;
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 actising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.
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                                                                                                                                                                               human monoclonal antibody that binds to platelet-derived cor-D (PDGF-D), useful for treating chronic and recurrent asses, such as inflammation, autoimmunity and cancer.
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Pred. No. 2e-34;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 227; 255pp; English
                                                                                  Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keyt B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
  07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-2003; 2003WO-US029414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-2002; 2002US-0411137P
                                                                                  Feng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 107; Conservative
                                                                                Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP
                                                                                                                                            WPI; 2003-587119/55.
                                         (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004024098-A2
                                                                                Corvalan JRF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                       Bezabeh B;
                                                                                                                                                                                                                            diseases,
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                                                                                                                                                                                                      Factor-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                           Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                        New human monoclonal antibody that binds to platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                       antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                           Gazit G,
Anti-human PDGF-D antibody protein related sequence #99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-human PDGF-D antibody protein related sequence #29.
                                                                                                                                                                                                                                                                                                                         Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 558; DB 7; 100.0%; Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 297; 255pp; English
                                                                                                                                                                                                                                                                                                                           Yang X,
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                                                                                                                                                                                                                                                                                                                         Feng X,
                                                                                                                                                                                                      06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                           07-JAN-2002; 2002US-00041860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                       Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107 AA;
                                                                                                                       WO2003057857-A2
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                                                                                Homo sapiens
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                                                                                                                                                            17-JUL-2003
                                                                                                                                                                                                                                                                                                                                              Bezabeh B;
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Query Match

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ADK18803

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Gaps

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Length 107;

9 9

107

Lichenstein H;

N-PSDB; ADL25413

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The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation, and (4) a method of treating mesangial cell proliferation, and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAA) variable region sequence, which is used in the exemplification of the present invention.
                                                   Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 107;
                                                                                                                                                                 Disclosure; SEQ ID NO 24; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                                             nephritis
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9 9 1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS Gaps ö RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107 0; Indels 100.0%; Score 558; DB 8; 100.0%; Pred. No. 2e-34; iive 0; Mismatches C Local Similarity 100. Les 107; Conservative 61 Best Loca Matches 셤 8 a

Human anti-EPO-R antibody light chain variable region SEQ ID NO:53 ADS84414 standard; protein; 107 AA (first entry) 18-NOV-2004 ADS84414; RESULT 7 ADS84414 

human; erythropoietin receptor; BPO receptor; erythropoietin receptor binding antibody; erythropoietin receptor binding antibody; EPO receptor binding antibody; antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia; wound healing; neural cell damage protection; neural tissue damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

WO2004035603-A2 Homo sapiens

29-APR-2004.

14-OCT-2003; 2003WO-US032243.

14-OCT-2002; 2002US-00269711. 10-OCT-2003; 2003US-00684109.

(ABBO ) ABBOTT LAB

Reilly EB, Wieler J; Ostrow DH, Devries PJ, Green LL,

WPI; 2004-348433/32. N-PSDB; ADS84413 New antibodies that bind to or activate an endogenous human

The present invention describes an antibody of the interpretaction of a cativates an endogenous activity of a human erythropotetin (EPD)

receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS&4362). Also described: (1) methods of medulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a computed for the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynuclectide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and composition and their fragments. The EPO receptor binding antibody has antianaemic, neuroprotective and vulnerary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dystunctional EPO receptor. The composition may also be used in the present sequence resulting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the chain variable region, which is given in the exemplification of the The present invention describes an antibody or its fragment that binds to erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g. Claim 10; SEQ ID NO 53; 192pp; English. present invention. anemia. 

Gaps ; 0 Length 107; 1; Indels Score 542; DB 8; Pred. No. 3.1e-33; 2; Mismatches 1; 97.1%; Matches 104; Conservative Query Match Best Local Similarity

Sequence 107 AA;

1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS

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> RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107 g 8

ADR68556 standard; protein; 107 RESULT 8 ADR68556

ADR68556;

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(first entry) 02-DEC-2004 Anti-EPO-R-antibody light chain variable region seqid 53.

antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; BPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; stroke; anti-EPO-R-antibody; light chain; variable region 

Homo sapiens

JS2004175379-A1

09-SEP-2004

10-OCT-2003; 2003US-00684109.

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                                                                                                                                                                                                                                                                                   The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin creceptor in a mammal, or that comprises at least one heavy or light chain creceptor in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification on its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also given in the specification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a mammal; a pharmaccutical composition comprising a therapeutic amount of mammal; a pharmaccutical composition comprising a 22-370 bp (even SEQ ID NO: 2-56) given in isolated and purified polynucleotide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NO: 9-56) given in the specification, and their fragments, complements, and degenerate codon cquivalents; and an isolated and purified amino acids sequence selected from 39 sequences comprising 27-552 amino acids (ad SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or their fragments. The antibody or its antibody or its antibody or its antibody or its antibody or complements are also useful for treating disorders characterised by decreased or subnormal levels of corygen in the blood or tissue such as hypoxaemia or chronic tissue corygen in the blood or tissue such as hypoxaemia or chronic tissue changed protecting against neural cell and/or tissue damage, resulting from the protecting against neural cell and/or tissue damage, resulting from coryceting against neural cell and/or tissue damage, resulting from coryceting application and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional cord injury, stroke and the like The antibodies are also cuseful for identifying or diagnosing mammals are also used a manine cortic transitional cord injury. S
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                                                                                                                                                                                                                 activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                         Wieler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                  antibody or its antibody fragment that activates an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 542; DB 8;
Pred. No. 3.1e-33;
2; Mismatches 1;
                                                                                                                         Green LL,
                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 53; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -antibody light chain variable region.
                                                                                                                         Reilly EB,
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14-OCT-2002; 2002US-0418031P.
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97.2%;
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                                                                                                                         Ostrow DH,
                                            OSTROW D H. REILLY E B.
                               DEVRIES P J
                                                                                                                                                      WPI; 2004-661369/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                         GREEN L L.
                                                                                         WIELER J.
                                                                                                                                                                     N-PSDB; ADR68555
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                                                                                                                     Devries PJ,
                                                          (REIL/)
(GREE/)
(WIEL/)
                               DEVR/)
                                               OSTR/)
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ID ADSE
XX AC ADSE
XX IB-1
XX DT 18-1
XX DE HUME
XX
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Human anti-BPO-R antibody Ab467 light chain SEQ ID NO:109.

(first entry)

18-NOV-2004 ADS84470;

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The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (BPO)

CC receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (BEQ ID NO:1, ADS04362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO cc receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from a plasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or its fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments or isolated and degenerate codon equivalents; and (5) an isolated and burified polynucleotide sequence, and their fragments. The EPO receptor complements and degenerate codon equivalents; and (5) an isolated and con be used in gene therapy. The compositions and methods activities, and can be used for modulating an endogenous activities, and can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from applasia or anaemia. They may also be used for identifying mammals having a dysfunctional and properting and properting mammals or anaemia.
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human; erythropoietin receptor; EPO receptor; erythropoietin receptor binding antibody; erythropoietin receptor binding antibody; antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor; e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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                                                                                                                            wound healing, neural cell damage protection;
neural tissue damage protection; brain injury; spinal cord injury;
stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQGTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 542; DB 8; Length 234; 97.2%; Pred. No. 6.4e-33; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wieler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reilly EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 109; 192pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ostrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-2002; 2002US-00269711.
10-OCT-2003; 2003US-00684109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-2003; 2003WO-US032243
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Sequence 234 AA;

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New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
                                                                                            antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
                                                                                                                                                                                                                                                                                                                          Reilly EB, Green LL, Wieler J;
                                                                           Human antibody Ab467 light chain polypeptide segid 109.
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 109; 156pp; English.
                  ADR68612 standard; protein; 234 AA.
                                                                                                                                                                                                                           10-OCT-2003; 2003US-00684109.
                                                                                                                                                                                                                                             14-OCT-2002; 2002US-0418031P
                                                       02-DEC-2004 (first entry)
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                                                                                                                                                                                                                                                                         OSTROW D H. REILLY E B. GREEN L L.
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N-PSDB; ADR68610.
                                                                                                                                                                                                                                                                 DEVRIES P J.
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                                                                                                                                                                                     US2004175379-A1.
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                       09-SEP-2004.
                                     ADR68612;
                                                                                                                                                                                                                                                                                      (REIL/)
(GREE/)
                                                                                                                                                                                                                                                                 DEVR/)
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                                                                                                                                               AB467
RESULT 10
         ADR68612
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The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin receptor in a mammal, or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ ID NO: 3 or 5) given in the specification or its fragment, but does not interact with a peptification and or its fragment, but does not interact with a peptification. Also described are: a method of activating or modulating an endogenous activity of a human erythropoietin receptor in a manibody or antibody fragment above and a pharmaccutical excipient; an isolated and purified polynucleotide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in the specification, and their fragments, complements, and degenerate codon equivalents; and an isolated and purified amino acids (ad SEQ ID NOs between SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or medulates the activity of the receptor is useful in a method of treating a mammal suffering aplasia or anamia. The antibodies are also useful for treating disorders characterised by decreased or subnormal levels of oxygen in the blood or tissue such as hypoxaemia or chronic tissue hypoxia and/or diseases characterised by inadequate blood circulation or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also esful for identifying or diagnosing mammals having dysfunctional erychropoietin receptor. This sequence represents a human Ab467 antibody light chain polypeptide.

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The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (BPO)

Creceptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human BPO receptor in a mammal, comprising administering to the mammal a creativate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polymucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The BPO receptor binding antibody has antianaemic, neuroprotective and vulnerary
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                                                                                                      21 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor binding antibody;
therapy; aplasia; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g.
                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; erythropoietin receptor; EPO receptor; erythropoietin receptor binding antibody; EPO receptor binding antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; ana wound healing; neural cell damage protection; spinal cord injury; etissue damage protection; brain injury; spinal cord injury; etroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-EPO-R antibody light chain variable region SEQ ID NO:41
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                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                        RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQGTKLEIK 127
  Score 542; DB 8; Length 234;
Pred. No. 6.4e-33;
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                                       1; Indels
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                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                            ADS84402 standard; protein; 107 AA
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10-OCT-2003; 2003US-00684109.
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  97.18;
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                                              Conservative
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Query Match
Best Local Similarity
Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                                    ADS84402;
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variable region having a sequence comprising 116 or 107 amino acids (SEQ ID No: 3 or 5) given in the specification or its fragment, but does not interact with a peptide comprising 30 amino acids (SEQ ID No: 1) also given in the specification. Also described are: a method of activating or

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activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human BPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-BPO-R antibody light chain variable region, which is given in the exemplification of the
                                                                                                                                                                                                                                                         1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxai; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; spinal cord injury; stroke; anti-EPO-R-antibody; light chain;
                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPCSFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-EPO-R-antibody light chain variable region segid 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wieler J;
                                                                                                                                                                                    Score 539; DB 8;
Pred. No. 5.2e-33;
3; Mismatches 1
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                                                                                                                                                                                     96.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                               Matches 103; Conservative
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OSTROW D H.
REILLY E B.
GREEN L L.
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                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                          Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2004
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(GREE/)
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New antibody or its antibody fragment that activates an endogenous activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.

N-PSDB; ADR68543

Claim 10; SEQ ID NO 41; 156pp; English.

The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin receptor in a mammal, or that comprises at least one heavy or light chain

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modulating an endogenous activity of a human erythropoietin receptor in a modulating an endogenous activity of a human erythropoietin receptor in a mathbody or antibody fragment above and a pharmaceutical excipient; an isolated and purified polynucleotide sequence selected from 28 sequences comprising 322-370 bp (even SEQ ID NOS between SEQ ID NOS 2-56) given in the specification, and their fragments, complements, and degenerate codon equivalents; and an isolated and purified amino acids sequence selected from 39 sequences comprising 27-55 amino acids (add SEQ ID NOS 3-57, and SEQ ID NOS 58-68) given in the specification or cheir fragments. The antibody or its antibody fragment that activates or modulates the activity of the receptor is useful in a method of treating a mammal suffering aplasia or anaemia. The antibodies are also useful for covygen in the blood or tissue such as hypoxaemia or chronic tissue or reduced blood flow. They are also useful for promoting wound healing or for protecting against neural cell and/or tissue damage, resulting from brain/spinal cord injury, stroke and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional cut in receptor. This is the amino acid sequence of an anti-BDO-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIXAASSLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 539; DB 8; Length 10
Pred. No. 5.2e-33;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anti-EPO-R antibody Ab390 light chain SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human, erythropoietin receptor; BPO receptor; erythropoietin receptor binding antibody; BPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS84452 standard; protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.6%;
96.3%;
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Best Local Similarity 96.3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 AA;
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The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (BPO) receptor in a mammal, but does not interact with a peptide having a creceptor in a mammal, but does not interact with a peptide having a creceptor in a mammal. MOS:, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human BPO creceptor in a mammal. comprising administering to the mammal a creceptor; (2) a method of treating a mammal suffering from activate the receptor; (2) a method of treating a mammal suffering from cativate the receptor; (2) a method of treating a mammal suffering from companiesting administering to the mammal a therapeutic amount of the above antibody or its fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified polynucleotide sequence, and their fragments. Complements and degenerate codon equivalents; and (5) an isolated and con be used in gene therapy. The compositions and methods activities, and can be used in gene therapy. The compositions and methods activities, and can be used for modulating an endogenous cativities, and a busy and so be used for identifying mammals having activity of a human BPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a receptor in properting and any and any and any any also be used in any and also be used in any any and any and any and any any and any and any and any and any any and any any and any any and any a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, etroke and the like. The present sequence represents a human anti-EPO-R antibody light chain, which is given in the exemplification of the present invention.
                                                                                                            New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g.
                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 91; 192pp; English.
                                                                                                        New antibodies that bind to
                                    N-PSDB; ADS84450, ADS84451
                                                                                                                                                                                                                                        anemia.
%XX4FFFFXXXXCCCCCCCCCCCCCCXXXXFFFFFXXXXX
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Sequence 234 AA;

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                                                                                                  21 DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                              1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                         Gaps
                                         ..
                                                                                                                                                                            81 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQTKLEIK 127
                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
96.6%; Score 539; DB 8; Length 234; 96.3%; Pred. No. 1.1e-32; ive 3; Mismatches 1; Indels
                                         Matches 103; Conservative
                     est Local Similarity
   Query Match
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ADR68594 standard; protein; 234 AA ADR68594; 

02-DEC-2004 (first entry)

Human antibody Ab390 light chain polypeptide seqid 91.

antianaemic; respiratory; vulnerary; gene therapy; vaccine; erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia; hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow; wound healing; neural cell damage; tissue damage; brain injury; spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain; AB390; ds

Homo sapiens

US2004175379-A1.

09-SEP-2004.

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The invention describes an antibody or its fragment that activates an endogenous activity or capable of binding to a human erythropoietin candogenous activity or that comprises at least one heavy or light chain variable region having a sequence comprising 116 or 107 amino acids (SEQ CO 1D NO: 3 or 5) given in the specification or its fragment, but does not given in the specification. Also described are: a method of activating or manmal; a pharmaceutical composition comprising a therapeutic amount of an antibody or antibody fragment above and a pharmaceutical excipient; an antibody or antibody fragment above and a pharmaceutical excipient; an antibody or antibody fragment above and a pharmaceutical excipient; an antibody or antibody fragment showe and a pharmaceutical excipient; or isolated and purified sequence selected from 28 sequences comprising 32-370 bp (even SEQ ID NO 80-25-56) given in the specification, and their fragments, complements, and degenerate codon comprising 27-552 amino acids (odd SEQ ID NOS between SEQ ID NOS 3-57, and SEQ ID NOS 5-52 amino acids (odd SEQ ID NOS between SEQ ID NOS 5-52 amino acids (odd SEQ ID NOS between SEQ ID NOS 3-57, and SEQ ID NOS 5-68 given in the specification or their fragments the activity of the receptor is useful in a method of treating alsorders characterised by decreased or subnormal levels of creating disorders characterised by decreased or subnormal levels of oxygen in the bload or tissue such as hypoxaemia or chronic tissue cyproced in and/or diseases characterised by inadequate bload circulation or reduced bload flow. They are also useful for promoting wound healing or brain/spinal cord injury, stroke and the like. The antibodies are also useful for identifying or diagnosing mammals having dysfunctional cypromotion and injury, stroke and the like. The antibodies are also the promoting and and promoting mammals baying dysfunctional cypromoting mammals and and promoting mammals and an antibod flow. They are also useful for promoting dysfunctional cypromoting a
                                                                                                                                                                                                                                                                                                                                                                                                                activity or is capable of binding to a human erythropoietin receptor in a mammal, useful for treating a mammal suffering aplasia or anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                New antibody or its antibody fragment that activates an endogenous
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                                                                                                                                                                                                                                                                        Reilly EB, Green LL, Wieler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 91; 156pp; English
                       10-OCT-2003; 2003US-00684109.
                                                                       14-OCT-2002; 2002US-0418031P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 96.3
Matches 103; Conservative
                                                                                                                                                                                                                                                                        Ostrow DH,
                                                                                                                   DEVRIES P J.
OSTROW D H.
REILLY E B.
GREEN L L.
                                                                                                                                                                                                                                                                                                                      WPI; 2004-661369/64.
N-PSDB; ADR68592.
                                                                                                                                                                                                                       WIELER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 234 AA;
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(REIL/)
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9 21 DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 80 61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107 81 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQGTKLEIK 127 ADK18841 standard; protein; 107 AA. (first entry) 06-MAY-2004 ADK18841; RESULT 15 ADK18841

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platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 306641880.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                          Weber R;
                                                                                                                                                                                                                                                                                                                                                                                           New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human monoclonal antibody that binds to
                                                   antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                          Gazit G,
                Anti-human PDGF-D antibody protein related sequence #67.
                                                                                                                                                                                                                                                                                                        Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 265; 255pp; English
                                                                                                                                                                                                                                                                                                 Corvalan JRF, Jia X, Feng X, Yang X,
                                                                                                                                                                                            06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                 07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                    (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107 AA;
                                                                                                                        WO2003057857-A2
                                                                                       Homo sapiens
                                                                                                                                                           17-JUL-2003.
                                                                                                                                                                                                                                                                                                                       Bezabeh B;
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Search completed: April 25, 2007, 04:05:19 Job time : 93.7938 secs

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Gaps

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Query Match
94.6%; Score 528; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 3.5e-32;
Matches 102; Conservative 3; Mismatches 2; Indels

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5.2.1	Biocceleration Ltd.
enCore version 6.2.1	- 2007 E
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

April 25, 2007, 04:05:37 ; Search time 8 Seconds (without alignments) 1261.509 Million cell updates/sec Run on:

US-10-665-383-24

Title: Perfect score:

1 DIQMTQSPSSLSASVGDRVT......CLQHNSDPCSFGQGTKLEIR 107 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		de				
Result		Query				
No.	Score	Match	Length	DB.	ΩI	Description
	501	8.68	125	7	S40353	Ig kappa chain V-J
7	494	88.5	108	٦	KIHUGL	kappa
m	489		108	г	KIHUWE	kappa
4	488	87.5	123	7	S40313	Ig kappa chain V-J
2	484	86.7	107	7	836269	Ig lambda chain V
9	481	9	117	~	S41809	kappa c
7	480	86.0	107	~	S36262	lambda
80	471	84.4	129	7	S40369	kappa c
0	468	83.9	123	7	S40331	Ig kappa chain - h
10	467	83.7	127	7	S40367	Ig kappa chain V-J
11	466	83.5	126	7	840335	kappa c
12	463	83.0	108	0	836279	Ig lambda chain V
13	463	83.0	108	0	B49047	Ig kappa chain V r
14	461	82.6	131	~	840352	kappa
15	460	82.4	114	N	846377	Ig kappa chain V-J
16	459	82.3	125	~	S40333	kappa
17	456	81.7	108	~	S19674	Ig kappa chain V r
. 18	455.5	81.6	107	~	S36275	Ig lambda chain V
19	455	81.5	108	Н	K1HUHU	kappa
20	455	81.5	125	N	S40349	
	454	81.4	95	N	868698	kappa
22	453	81.2	132	~	S40334	Ig kappa chain - h
	452	81.0	117	N	842264	Ig kappa chain V r
	ın	80.8	117	~	S46376	Ig kappa chain V-J
25	450.5	80.7	107	N	S47183	Ig kappa chain - h
	4	ö	107	~	169017	anti-HIV1 envelope
	4	。	129	-	$\overline{}$	shain
28	447.5	80.2	124	~	4	
29	447	80.1	107	~	836264	

Ig kappa chain V-I	Ig kappa chain - h	Ig kappa chain V r	Ig kappa chain V-I	Ig kappa chain - h	Ig lambda chain V	Ig kappa chain V-J			kappa	Ig kappa chain V-J	kappa	kappa	light	Ig kappa chain V r	Ig kappa chain - h
KIHUEU	S47182	S52793	K1HUBN	S40317	S36266	S46371	S44122	S40314	830521	S46370	C21056	S40318	S46372	S52789	831998
08	08 2	29 2	08 1	29 2	05 2	117 2	08 2	22 2	08 2	20 2	17 2	24 2	28 2	29 2	09 2
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-		7	46	46	145	445	444	444	13.5	443	442	441	441	438	437
	447	44	4	4	4	•			4						•

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C; Species: Home sapiens (man)
C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Date: 19-May-1994
R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Fitle: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: $40312; WUDD:94080891; PMID:8258341
A; Reference number: $40312; WUDD:94080891; PMID:8258341
A; Reference preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-125 cKLE>
A; Cross-references: UNIPARC:UPI0000176CAE; EMBL:X72463
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 501; DB 2; Length 14.
Pred. No. 3.2e-36;
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Ig kappa chain V-J-C region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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15 DIQMTQSPSSLSASVGDRVTITCRASQGIGNDLGWYQQKPGKAPKRLIYAASSFQSGVPS 74 61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107 셤 ð

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Ig kappa chain V-I region (Gal) - human (tentative sequence)

Cispecies: Hono sapiens (man)
Cispecies: Hono sapiens (man)
Cispecies: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004
Cipace: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004
Cipacesion: A01867
Ailaure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1564, 1973
Airlie: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I.
Airlie: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I.
Airlie: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I.
Airlie: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I.
Airlie: The primary structure of a monoclonal IgM-immunoglobulin.
Airlie: This chain was isolated from a Waldenstrom's macroglobulin.
Cigenetics:
Aircoss-references: GDB:136264
Aircoss-references: GDB:136264

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hain disulfide bords. In some cases, such as IgA and IgM, the subunits associate into la C, Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A;Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA)
A;Reference number: A93964; MUID:83273707; PMID:6410398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:P01610; UNIPARC:UP1000012E14C; Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGAGTEFTLTISSLQPEDFATYYCLQQNSYPRSFGGGTKVEIK 107
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                                                                                                                                                                   ch 88.5%; Score 494; DB 1; Length 108; 1 Similarity 89.7%; Pred. No. 1.1e-35; 96; Conservative 5; Mismatches 6; Indels
                                                                      C; Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;16-90/Domain: immunoglobulin homology <IMM>F;23-88/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-I region (WEA) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V-J region - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-108 <GON>
                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: GDB:IGKV1
                                                                                                                                                                           Query Match
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Matches
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A;Cross-references: UNIPARC:UPI000011613F; EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF1; EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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R,Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zaci Bur. J. Immunol. 23, 2868-2875, 1993
A;Tit.le: The V(Kappa) genes of the L regions and the repertoire of V(kappa) gene sequence A;Feference number: S41809
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-117 <HUB>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O3-Feb-1994 #sequence_revision O3-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, JEMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36265; MUID:93178448; PMID:7679990
A;Accession: S36269
A;Status: preliminary; nucleic acid sequence not shown
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRESQGIRNDLGWYQQKPGKAPKLLIYGTSSLQSGVPS
                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Feywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                               Indels
                                                                                                                                                 Score 488; DB 2; L. Pred. No. 4.1e-35; 7; Mismatches 6;
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Pred. No. 1.6e-34;
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1 Similarity 87.9%;
94; Conservative '
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Best Local Similarity
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Best Local S
Matches 94
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Matches
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A;Cross-references: UNIPARC:UP10000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                 Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40335
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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Pred. No. 2.1e-33;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 127;
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A;Cross-references: UNIPARC:UP10000176CB4; EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
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86.0%; Pred. No. 2.7e-33;
ive 5; Mismatches 10
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.9%;
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Matches 93; Conservative
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nes 92; Conservative
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Best Local S:
Matches 92
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S40335
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                                                                                                                                                                                                                                                                                                               Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: 83622
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. RshBo J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: 836256; MUID:93178448; PMID:7679990
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $4036 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $4036 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Ext. J. Immunol. 23, 3248-3271, 1993
A;Ritle: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40369
A;Reference number: $40369
                                                                           23 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UP10000176D2C; EMBL:Z18842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                          83 RFSGSGGTEFTLTISSLQPEDFATYYCLQHNSYP 117
                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDP 95
  Mismatches
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  1,
  Conservative
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nes 94; Conservative
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Best Local Similarity
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A; Residues: 1-107 <GRI>
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A; Residues: 1-129 < KLE>
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93;
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  Matches
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A;Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Pis C;Keywords: heterotetramer; immunoglobulin P;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                         1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIQMTQSPSSLSASVGNRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                     1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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A; Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
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R, Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 2348-3271, 1993
A, Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIK 107
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                                                                                                                     Length 108;
                              C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                               83.0%; Score 463; DB 2; Length 10
86.0%; Pred. No. 5.1e-33;
ive 4; Mismatches 11; Indels
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A;Accession: S40352
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82.6%; Score 461; DB 2;
Best Local Similarity 84.1%; Pred. No. 9e-33;
Matches 90; Conservative 8; Mismatches
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EMBO J. 13, 2951-2962, 1994
                                                                                          Query Match
Best Local Similarity 86.0-
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Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
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A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Emboro. 12, 725-734, 1993
BMSO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40335
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R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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83.5%; Score 466; DB 2; Length 12
Best Local Similarity 84.9%; Pred. No. 3.2e-33;
Matches 90; Conservative 8; Mismatches 8; Indels
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      Immunol. 23, 3248-3271, 1993
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Matches 90; Conserv
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A;Residues: 1-126 <KLE>
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A, Residues: 1-114 cBEN>
A, Residues: 1-114 cBEN>
A, Cross-references: UNIPARC:UPI00001165AA; EMBL: Z27178; NID: 9415971; PIDN: CAA81702.1; PII
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Reywords: heterotetramer; immunoglobulin
F;22-96/Domain: immunoglobulin homology <IMM>
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                                                                     C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46377; S38650
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S46377
Ig kappa chain V-J region (T33-17) - human (fragment)
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8 IQMRQSPSSLSASVGDRVTITCRASQGIRNDLGWNQQKPGKAPKLLIYAASSLESGVPSR 67

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62 FGGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEI 106

Search completed: April 25, 2007, 04:06:39 Job time : 9.16102 secs

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NCBI_TaxID=9606;
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0502W4;
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Q6gmxy
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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KVIR HUMAN
Q9UL70 HUMAN
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Q9UL81 HUMAN
KV10 HUMAN
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Q6PIH4 HUMAN
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KV1V_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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KV1C HUMAN
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                                                                                                                Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                 UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                          US-10-665-383-24
                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                         BLOSUM62
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                                                                                  Perfect score:
                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                              446
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P01594 homo sapien P80362 homo sapien P01596 homo sapien P01604 homo sapien Q7z473 homo sapien P01693 homo sapien P01608 homo sapien P01602 homo sapien P01602 homo sapien P01602 homo sapien P01652 mus musculu Q56917 homo sapien Q56917 homo sapien	Forest nomo sapten
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MEDLINE-22388257, PubMed=12477932, DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetev K.H., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetev K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rapleton M.J., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
Robards S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.M., Krzywinski M.I., Shalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini;
Catarrhini; Hominidae, Homo.
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-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                    UniProtKB/TrEMBL.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
    236 AA.
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    PRT;
                                                                                07-JUN-2005, integrated into Unil 07-JUN-2005, sequence version 1. 11-JUL-2006, entry version 13.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednences."
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QGGMW1_HUMAN PRELIMINARY; PRT;
QGGMW1;
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               PROSITE; PS50835; IG LIKE; 1.
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Proc. Natl. Acad. Sci. U.
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les 96; Conserv
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Name=IGKC;
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               ð
GO; GO: 0030106; F:MHC class I receptor activity; IEA.

GO; GO: 0019883; P:antigen presentation, endogenous antigen; IEA.

R GO; GO: 0109883; P:antigen precessing, endogenous antigen via . .; IEA.

R INTERPRO; IPR00310; IG-like.

R INTERPO; IPR003106; IG-MHC.

R INTERPO; IPR003599; IG-Bet.

R INTERPO; IPR003599; IG-West.

R INTERPO; IPR003599; IG-V-set.

R INTERPO; IPR003596; IG-V-set.

R INTERPO; IPR003596; IG-V-set.

R RAMRT; SM00406; IG-Set; I.

SMART; SM00406; III-Set; II-

SMART; SM00406; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-75059122; PubMed=4215718;
MEDLINE-75059122; PubMed=4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";
Hoppa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANEQUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEQUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%; Score 511; DB 2; Length 236; 91.6%; Pred. No. 2.1e-44; Live 7; Mismatches 2; Indels
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Ig kappa chain V-I region Gal.
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InterPro; IPR003599; Ig sub. InterPro; IPR003599; Ig V-set.
InterPro; IPR003596; Ig_V-set.
Ffam; PF07686; V-set; 1.
SWART; SW00409; IG; 1.
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Matches 98; Conservative
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SMR; P01599; 1-108.
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DER NEUER PRESENTATION OF THE PRESENTATION OF

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Turbulespieder R. L., Feingold E.A., Grouse L.H., Derge J.G., Klausberg, Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Schaefer C.F., Bhat N.K., And Lischul E.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Usdin T.B., Enando M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Ponaldo M.F., Carninci P., Prange C., Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Robsak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abosak S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A., Andelton B.X., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mullalon D.X., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mullalon D.X., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., All M. Marna M. M. Anderston M. Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGAGTEFTLTISSLQPEDFATYYCLQQNSYPRSFGGGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
                                                                            Ig kappa chain V-I region Gal.
/FTId=PRO 0000059743.
                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-3. Framework-4. By similarity.
                                                                                                                                                                                                      Complementarity-determining-1.
                                                                                                                                                                                                                                                                                   Complementarity-determining-2.
                                                                                                                                                         23 Framework-1.
34 Complementarity-determining-
49 Framework-2.
56 Complementarity-determining-
88 Framework-3.
97 Complementarity-determining-
107 Framework-4.
88 By similarity.
88 By similarity.
81 RM, ClAD3CB0F600FF73 CRC64;
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Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.

CHAIN I >108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.5%; Score 494; DB 1;
ilarity 89.7%; Pred. No. 4.9e-43;
Conservative 5; Mismatches 6;
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| R EMBL; | EC073791; | A4H73791.1; -; | mRNA. |
| R EMBL; | ENSG0000163245; | Homo sapiens. |
| R GO; | GG; | C016021; | C:integral to membrane; | IEA. |
| GO; | GO: 0016020; | C:membrane; | IEA. |
| GO; | GO: 0019081; | P:mHC class I receptor activity; | IEA. |
| GO; | GO: 0019081; | P:mtigen presentation, endogenous antigen via . .; | IEA. |
| R GO; | GO: 0019081; | P:mtigen processing, endogenous antigen via . .; | IEA. |
| R InterPro; | IPR00310; | Ig MHC. |
| R InterPro; | IPR003106; | Ig MHC. |
| R InterPro; | IPR003106; | Ig WHC. |
| R InterPro; | IPR003106; | Ig V-set. |
| R InterPro; | IPR003106; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R InterPro; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IPR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | IRR003569; | Ig V-set. |
| R INTERPRO; | IRR003569; | IRR003569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody against 3.4-pyruvylated galactose and isolated from a patient with Waldenstrom's macroglobulinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGRAPKLLIYAASSLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  histocompatibility complex class I molecules (By similarity).
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O-MAY-2006, entry version 39.

Ig kappa chain V-I region WEA.

Homo sapiens (Human).

Bukaryotes, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%; Score 490; DB 2; Length 236; 90.6%; Pred. No. 3.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00409; IG; 1.
SMART; SM004007; IGc1; 1.
SMART; SM004007; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNRNOWN 1.
Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 236 AA; 25751 MW; SBFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.6
nes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF07654; C1-set; 1. Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01876; K1HUWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P80362; 1WTL.
SMR; P01610; 1-108.
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P01610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ID KVIR HUMAN

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01-MAY-2000, sequence version 1.
18-APR-2006, entry version 23.
Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKKLIYGATSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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MEDLINE-92078875; PubMed-1660528; DOI=10.1084/jem.174.6.1639;
Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characteristics of antibodies bearing an anti-DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 489; DB 1; Length 108;
Pred. No. 1.6e-42;
9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                           Ig kappa chain V-I region WEA. /FIId=PRO 0000059752.
                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Framework-3.
Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11840 MW; 9249B61F0945618C CRC64;
                                                                   InterPro; IPR007110; Ig-like.
InterPro; IRR003599; Ig_sub.
InterPro; IPR013106; Ig_v.set.
InterPro; IPR013106; Ig_v.set.
InterPro; IPR013566; Ig_v.set_sub.
Pfam; PP07686; V-8et; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IG; 1.
PR051TE; PS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998)
  NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
GO; GO:0005576; C:extracellular region; GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF035044; AAD56280.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Exp. Med. 174:1639-1652(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhin; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.98;
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ses 93; Conservative
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34
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56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diamond B.;
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histocompatibility complex class I molecules (By similarity).
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DDT TDD DDT DD
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
B Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nollalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,
A Nollalon D.K., Muzny D.W., Sodergren B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield W. Schein J.E., Jones S.J.M., Marra M.A.;
Butenfield M. Schein J.E., Jones S.J.M., Marra M.A.;
Butterfield W. Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIÓMTÓSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%; Score 469; DB 2; Length 108;
86.0%; Pred. No. 1.9e-40;
tive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                     108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA.
                                                                    InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig sub.
InterPro; IPR003599; Ig sub.
InterPro; IPR003596; Ig V-set.
InterPro; IPR003596; Ig V-set.
Pfam; PP07686; V-set; 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGMX8_HUMAN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2004, sequence version 1. 27-JUN-2006, entry version 22. IGKC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 86.0 tes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
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NIH MGC Project;
                                                                                                                                                                                                                                                                                        Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] TOUTEOTIDE SEQUENCE
  PIR; PH0863; PH0863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                           HSSP; P01607; 1BWW
SMR; Q9UL70; 1-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                               108
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=IGKC;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGGMX8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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M. GO, GO: 0016021; C:integral to membrane; IEA.

RG GO: GO: 0016020; C:membrane; IEA.

RG GO: 0016020; C:membrane; IEA.

RG GO: 0016020; C:membrane; IEA.

RG GO: 00108081; P:antigen presentation, endogenous antigen; IEA.

RG GO: GO: 0019885; P:antigen presentation, endogenous antigen; IEA.

RG GO: GO: 0019885; P:antigen presentation, endogenous antigen; IEA.

RG GO: GO: 0019885; P:antigen presentation, endogenous antigen; IEA.

RG GO: GO: 0019885; P:antigen presentation, endogenous antigen; IEA.

RITERPRO; IPR001359; Ig_Cl-set.

RITERPRO; IPR001359; Ig_Cl-set.

RITERPRO; IPR001359; Ig_V-set.

RITERPRO; IRR001359; Ig_V-set.

RITERPRO; RR001405; Ig, I.

RR Ffam; PR076654; Cl-set; I.

RR RART; SM00409; IG; I.

RR SMART; SM00406; IGV; I.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSDERG R.L., Feingold B.A., Grouse L.H., Derged J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

MISCHIL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

MISCHOL, Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFGOGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 462; DB 2; Length 23.
05 0%; Pred. No. 2.5e-39;
07 0%; Pred. No. 2.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPFTFGPGTKVDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MCF, UNKNOWN 1.
Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003, integrated into UniProtKB/TrEMBL. 01-OCT-2003, sequence version 1. 27-UNV-2006, entry version 25. 37-UNV-2006, entry version 25. Homo sapiens (Human)
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Q7Z3Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%; Pred. ...
                                                                                                                                                                                                     Ensembl; ENSG0000163245; Homo sapiens.
                                                                                                                         ; BC073764; AAH73764.1; -; mRNA.
QGGMX8; 24-235.
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chain of subgroup I (Bence-Jones protein Hau): subdivision within
               subgroups.
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DISULFID
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                                                                                                                                                                                                           HISSP; PO1834; JHEZ.

R Ensembl; ENSGO000161245; Homo sapiens.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0018629; C:membrane; IEA.

GO; GO:0019883; P:antigen precessing, endogenous antigen; IEA.

GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.

InterPro; IPR003597; Ig_Cl-set.

R InterPro; IPR003599; Ig_Cl-set.

R InterPro; IPR003599; Ig_Cl-set.

R InterPro; IPR003599; Ig_Wb.

R InterPro; IPR003599; Ig_Wb.

R InterPro; IPR003599; Ig_V-set.

R PRAM; PF07654; Cl-set; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIOMTOSPSSLSASVGDTVTITCRASQDISNYLAWFOOKPCKAPKSLIYGASSLOSGVOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=71032830; PubMed=4097974;
Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin L-
                                                                                                                  Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 81.7%; Score 456; DB 2; Length 236; Similarity 84.1%; Pred. No. 1e-38; 90; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                              and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 25-JUL-2006, entry version 47. Ig kappa chain V-I region Hau. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA
                                                                                                                                                                                                   EMBL; BC005332; AAH05332.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSTIE; PSS0835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                               NUCLEOTIDE SEQUENCE.
TISSUE=Skeletal Muscle;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEOUENCE.
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P01600;
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                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.

CHAIN 1 >108 Ig kappa chain V-I region Hau.
/FIId=PRO_000059744.
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Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-2.
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Framework-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
11671 MW; 08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR013106; Ig_V-set.
Flam; PF07686; V-set; 1.
SMART; SM00409; IG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                1F6L; X-ray; L=1-89.
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Best Local Similarity 84.1
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; CHAIN
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34
49
49
56
88
97
107
108
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                             Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ne segments rearranged in chronic lymphocytic leukemia are over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=92337224; PubMed=1516616;
MEDLINE=92337224; PubMed=1516616;
Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
"Human monoclonal striational autoantibodies isolated from thymic B
lymphocytes of patients with myasthenia gravis use VH and VL gene
segments associated with the autoammune repertoire.";
Eur. J. Immunol. 22:2231-2236(1992).
                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleos
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini
                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                 01-MAY-2000, integrated into UniProtKB/TrEMBL
                          108 AA.
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PIR; S34083; S34083.
HSSP, P01607; 1BWW.
SMR; Q9UL77; 1-108.
Ensembl; ENSG0000163245; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035037; AAD56273.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Igsub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR013106; Ig-V-set.
Fam; PR07686; Vg-vset; 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IGv; 1.
PR0SITE; PS50815; IG_LIKE; 1.
Immunoglobulin domain.
NON_TER
                          PRT;
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Wagner S.D., Luzzatto L.;
W. Kappa gene segments rearranged
distributed over a large portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Immunol. 23:391-397(1993).
                                                                                       sequence version 1.
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                        PRELIMINARY;
                                                                                                                                                                                                                Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RZPD-ProtExp; IOH14191; ..
RZPD-ProtExp; IOH21663; ..
RZPD-ProtExp; IOH23035; ..
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                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somatic mutation.
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                        Q<u>9</u>UL77_HUMAN
09UL77;
                                                                                       01-MAY-2000,
                                                                                                           13-JUN-2006.
                                                                                                                                                                                                                                                                                                                                                                                          fetus."
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Richards R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altsusher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altsusher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetcow K.M., S.L., Wang J., Hsieh F., Dordan H., Moore T., Max. R.L., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdain T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Archards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnert A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                 1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                     1 DIOMTOSPSSLSASVGDRVTITCRASOSISSYLNWYQOKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                          Gaps
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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PDB; 2AJ3; X-ray; A/C/E=25-236.
SMR; 06P1H7; 23-236.
Ensembl; ENSG0000163245; Homo sapiens.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:001016020; C:membrane; IEA.
GO; GO:001016020; F:MHC class I receptor activity; IEA.
GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas_242603899;
                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
                                                                   Length 108;
                                                                                                                                          12; Indels
108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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                                                                   Score 453; DB 2;
Pred. No. 8.6e-39;
5; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 25-JUL-2006, entry version 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEPIH7_HUMAN PRELIMINARY; PRT;
Q6PIH7;
                                                                   81.2%;
84.1%;
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NCBI_TaxID=9606;
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                                                                                                            Similarity
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RZPD-ProtExp, T2901; -. RZPD-ProtExp, T2902; -. RZPD-ProtExp, W0370; -.
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129
129 AA;
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P01598;
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SEQUENCE
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KV1F HUMAN
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GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA. InterPro; IRR00310; Ig-like.
InterPro; IRR00310; Ig-Cl-set.
InterPro; IRR003006; Ig-MHC.
InterPro; IRR003599; Ig-sub.
InterPro; IRR003596; Ig-V-set.
InterPro; IRR003596; Ig-Set.
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Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.2%; Score 453; DB 2; Length 236; 83.2%; Pred. No. 2.1e-38; Artive 7; Mismatches 11; Indels
                                                                                                                                                                                SWART; SW00409; IG; 1.
SWART; SW00407; IGc1; 1.
SWART; SW00407; IGc1; 1.
PROSITE; PSC6835; IG LIKE; 2.
PROSITE; PSC6929; IG MHC; UNKNOWN 1.
Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 236 AA; 25603 MW; 8BCS61106861213F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987, integrated into UniProtKB/Swiss-Prot. 13-AUG-1987, sequence version 1. 27-UUN-2006, entry version 43. Ig kappa chain V-I region Walker precursor.
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                                                                                                                                                                                                                                                                                                                                                                                               89; Conservative
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IOH7177;
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Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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Bochemietry 9:1388-3196(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) mark.
-!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
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Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
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                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V-I region Walker.
/FTId=PRO 0000015170.
Framework-1.
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.5%; Score 449; DB 1; Length 129; 85.0%; Pred. No. 2.7e-38; ive 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-1
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                                                                                                                                                                                                                                                                               SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14069 MW; F941FA07D4AFC2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 40. Ig kappa chain V-I region EU.
GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig sub.
InterPro; IPR003599; Ig V-set.
InterPro; IPR003596; Ig V-set.
Fam; PF07686; V-set; 1.
SWART; SM004009; IG; 1.
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es 91; Conservative
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GO; GO:0003823; F:antigen binding; GO; GO:0006955; P:immune response:
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMIQSPSTILSASVGDRVTITCRASQSINITMLAWYQQKPGKAPKLLMYKASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
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"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
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Framework-1.
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                                                                          HESP: POLOGO: ALTHONO.

SMR: POLS99; 1-107.

BARSHD1; ENSGO000163245; Homo sapiens.

BARSHD1; ENSGO000163245; Homo sapiens.

GO: GO:0003823; F:antigen binding; NAS.

GO: GO:0005576; C:extracellular region; NAS.

GO: GO:000595; P:imune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003199; Ig-sub.

InterPro; IPR003599; Ig-sub.

InterPro; IPR003599; Ig-vset.

InterPro; IPR003599; Ig-vset.

InterPro; IPR003599; Ig-vset.

INTERPRO; IPR003599; Ig-vset.

Pfam; PR07686; V-set.; I.

SWART; SM00406; IG; I.

PROSITE; PSS0835; IG LIKE; I.

Direct, protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.AUG-1987, integrated into UniProtKB/Swiss-Prot.
13.AUG-1987, sequence version 1.
30.MAY-2006, entry version 41.
Ig kappa chain V-I region BAN.
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Pred. No. 3.6e-38;
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SWR; P04430; 1-108.
GO; GO:0005576; C:extracellular region; NAS.
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                                                              PIR; A90562; K1HUEU
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KV1V HIDAN

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1 DIQMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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"V kappa gene segments rearranged in chronic lymphocytic leukemia are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region (Fragment).
Homo sapiens (Hunan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
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01-DEC-2001, sequence version 1.
18-APR-2006, entry version 19.
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
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MEDLINE=98375893; PubMed=9712075;
Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis; human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
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InterPro; IPR007110; Ig-like.
InterPro; IPR0013106; Ig-like.
InterPro; IPR0013106; Ig-V-set_sub.
InterPro; IPR003596; Ig-V-set_sub.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
Amyloid; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
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                                                                                                                                                                                                                                                                                 Ig kappa chain V-I region BAN /FIId=PRO 0000059756.
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Pred. No. 4.6e-38;
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By similarity.
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MEDLINE=93170387; PubMed=8436174;
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Immunol. 161:2020-2031(1998).
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NCBI_TaxID=9606;
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distributed over a large portion of the V kappa locus and do not show somatic mutation."; Eur. J. Immunol. 23:391-397(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLAWYQQKPGKAPKLIYAASSLQSGVPS
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MEDLINE=91243737; PubMed=1903706;
MEDLINE=91243737; PubMed=1903706;
MEDLINE=91243737; PubMed=1903706;
Malaison G., Kuhtz J.L., Pasquali J.L.;
"Molecular analysis of V kappa III variable regions of polyclonal rheumatoid factors during rheumatoid arthritis.";
Eur. J. Immunol. 21:1221-1227(1991).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Haplorrhini,
                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 79.8%; Score 445.5; DB 2; Length 107; l Similarity 84.1%; Pred. No. 5.1e-38; 90; Conservative 5; Mismatches 11; Indels 1.
                                                                                                                "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
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107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                            PIR; S16840; 516840.
PIR; S31977; S31977.
PIR; S34083; S34083.
PIR; S34086; S34086.
HSSP; PO1607; IBWW.
SMR; Q965A9; 1-107.
LinkHub; Q96SA9; -.
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InterPro; IPR013599; Ig-sub.
InterPro; IPR013106; Ig-V-set.
InterPro; IPR03596; Ig-V-set_sub.
Pfam; PP07686; V-set, 1.
                                                                                                                                                                                                                                                                                                                     EMBL; U96396; AAB68785.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2004, sequence version 1.
18-APR-2006, entry version 10.
Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q65ZC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                  PIR; B49047; B49047.
PIR; PH0867; PH0867.
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                                                                                                   Diamond B.;
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Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

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                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629; Kontermann R.E., Wing M.G., Winter G.; "Complement recruitment using bispecific diabodies."; Nat. Biotechnol. 15:629-631(1997).
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Best Local Similarity 80.4%; Pred. No. 1.5e-3/;
Best Local Similarity 80.4%; Pred. No. 1.5e-3/;
Matches 86; Conservative 10; Mismatches 11; Indels
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                                                                                                                                                                                                               EMBL, Y13057; CAA73500.1; -; mRNA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR013196; Ig-ub.
InterPro; IPR013106; Ig-V-set_sub.
Fām; PF07686; V-set; 2.
SWART; SW00406; IG; 2.
SWART; SW00406; IGv; 2.
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18, Appli 3, Appli 12, Appli 12, Appli 1, Appli 1, Appli 1, Appli 10, Appli

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Sequence 24, Sequence 13, Sequence 32, Sequence 34, Sequence 8,

Sequence 3

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1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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Pred. No. 8.4e-42;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10330613A

Sequence 18, Application US/10330613A

Batent No. 6224360

GENERAL INFORMATION:
APPLICANT: Gudas, Jan

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTICEN

FILE REFERENCE: ABGENIX. 022A

CURRENT APPLICATION NUMBER: US/10/330,613A

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: 60/346299

; PRIOR RILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: ReatSEQ for Windows Version 4.0

; ENDING: 100 18
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Sequence 14, Application US/10330613A

Patent No. 6924360

GENERAL INFORMATION:

APPLICANT GUASA, Jean

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/330,613A

CURRENT PILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 90 10 12-18

SOFTWARE PARESEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 107
         US-09-602-812A-5
PCTT-US93-07832-18
US-08-994-07832-18
US-08-995-798-3
US-08-999-26-1
US-09-125-098-1
US-09-125-098-1
US-09-540-018-1
US-09-540-018-1
US-09-378-939-32
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US-08-378-939-24
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94.4%;
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Matches 101; Conservative
ORGANISM: Homo Sapiens
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TYPE: PRT
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1 DIOMTQSPSSLSASVGDRVT......CLQHNSDPCSFGQGTKLEIR 107
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/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-125-098-9

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Maximum Match 100%
Listing first 45 summaries
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Sequence 29, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT APPLICATION NUMBER: US/09/240,274

GEALIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN VET. 2.0
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GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SCRTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-420.
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 22.0
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Pred. No. 1.5e-38;
7; Mismatches 5; Indels
                                                               Score 519; DB 2; Length 107;
Pred. No. 3e-41;
4; Mismatches 3; Indels
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88.6%;
                                                             Query Match
Best Local Similarity 93.5%;
Matches 100; Conservative
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Best Local Similarity 88.57
These 93; Conservative
; ORGANISM: Homo Sapiens
US-10-330-613A-14
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LENGTH: 107
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1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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88.6%; Pred. No. 1.5e-38;
live 7; Mismatches 5; Indels
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Pred. No. 9.3e-38;
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APPLICANT: FOOTE, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 59
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                                                                          OTHER INFORMATION: anti-Rh(D) chain F01
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Patent No. 6881557
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97.9%;
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Best Local Similarity 88.6<sup>†</sup>
Matches 93; Conservative
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Best Local Similarity 97.9°
Matches 93, Conservative
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-10-194-975-59
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ORGANISM: Homo sapiens
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LENGTH: 95
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                                                   Gaps
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       Length 95;
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Pred. No. 9.3e-38;
1; Mismatches 1; Indels
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FILE REPRENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT PILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FRALESQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 95
                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
    Score 481; DB 2;
Pred. No. 9.3e-38;
1; Mismatches 1;
                                                                                                                                                                                                                 RFSGSGGTEFTLTISSLQPEDFATYYCLQHNSYP 95
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 95
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Patent No. 6924360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 51, Application US/10330613A; Patent No. 6924360; GENERAL INFORMATION:
    86.2%;
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Best Local Similarity 97.9%;
Matches 93; Conservative
                                                 93; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 93; Conserv
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US-10-330-613A-51
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Sequence 52, Application US/10330613A

Sequence 52, Application US/10330613A

Patent No. 6924360

Title REPERPLY: Gudas, Jean

TITLE REPERPLY: ABGENIX 0.22A

CURRENT FILICATION NUMBER: US/10/330,613A

CURRENT FILICATION NUMBER: 0.346299

PRIOR FILICATION NUMBER: 60/346299

PRIOR FILICATION NUMBER: 60/346299

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 5: SEQ ID NOS: 90

LENGTHARE: PastSEQ for Windows Version 4.0

LENGTH: 95
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APPLICANT: Schoenhaut, David
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Trietan J.
APPLICANT: Wilte, Michael
APPLICANT: Wilter, Wi
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDP 95
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Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
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60 State Street, suite 510
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Mankovich, John A.
McGuinness, Brian T.
Roberts, Andrew J.
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Best Local Similarity 97.33
Best Local Similarity 97.33
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STATE: Massachusetts
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6090382
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REFERENCE/DOCKET NUMBER: BBI-043
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STATE: Massac
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APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughaut, David
APPLICANT: White, Michael
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNPa
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIUP F. COLLEGE CONTROL OF CORPERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKVEIK 107
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.2%; Score 481; DB 2; Length 107; Best Local Similarity 86.9%; Pred. No. 1.1e-37; Matches 93; Conservative 7; Mismatches 7; Indels
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CONDUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakcalan, Zehra
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60 State Street, suite 510
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DECONTE, GIULIO A., Jr.
REGISTRATION NUMBER: 31,503
                                                                                                       BBI-043
                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
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Mankovich, John A.
McGuinness, Brian T.
  08-FEB-1996
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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STREET: by
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FILING DATE:
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APPLICANT:
APPLICANT:
APPLICANT:
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US-09-125-098-9
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1 DIQMIQSPSSLSASIGDRVIITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
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                                                                                                                                                                                                                                               Score 481; DB 2; Length 107;
Pred. No. 1.1e-37;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Wilton, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
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CURRENT APPLICATION DATA: US/09/540,018
FILING DATE: 31-MARCH-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salfeld, Jochen G.
Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
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FILING DATE: 31-MARCH-2000
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DECORET, GIULIA A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (G17)227-7400
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60 State Street, suite 510
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Mankovich, John A.
McGuinness, Brian T.
Roberts, Andrew J.
Sakorafas, Paul
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Patent No. 6509015
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                         86.2%;
86.9%;
                                                                       Query Match
Best Local Similarity 86.9°
Matches 93, Conservative
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                                                                                                                                                                MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-125-098-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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ADDRESSEE: LAHIVE &
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61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107

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                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKVEIK 107
                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
                                                                                                                     Score 481; DB 2; Length 107;
Pred. No. 1.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.0%; Score 480; DB 2; Length 109; Best Local Similarity 87.9%; Pred. No. 1.3e-37; Matches 94; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 139, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                      86.2%;
86.9%;
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                   1 Similarity 86.9 93; Conservative
                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                              linear
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-025-769B-28
                                              TOPOLOGY:
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                                                                                         US-09-540-018-9
                                                                                                                      Query Match
Best Local
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1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS

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1 DIQMIQSPSSLSASVGDRVIIITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 109;
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER TOTAL
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILLING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILLING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., ESG.
REGISTRATION NUMBER: 27,794
PROFINENTIAL NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                      E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                       APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 480; DB 2;
Pred. No. 1.3e-37;
5; Mismatches 8.
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; Sequence 43, Application US/09025769B
; Patent No. 6300064
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.0%;
87.9%;
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Best Local Similarity 87.95
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    ADDRESSEE:
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plucackthum, Andreas
Plucackthum, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 37
ADDRESSES: Colin G. Sandercock, Esq. c/O Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Relangeon
STREED: C.
COUNTRY: 105A
ZTR: 2006
COMPTRE: 105A
COMPTRE: Lab PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
COMPTRE: 11 MP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPRISED: Patentin WARDE: VG/ON/ON MADDRE: VG/ON/ON MADDRE: VG/ON/ON MADDRE: VG/ON/ON MADDRE: VG/ON/ON MADDRE: VG/ON/ON MADDRE: PG/ON/ON MADDRE: VG/ON/ON MA
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 Query Match
 86.0%;
 Score 480;
 DB 2;
 Length 109;

 Best Local Similarity 87.9%;
 Pred. No. 1.3e-37;
 Gaps
 0;

 Matches 94;
 Conservative 5;
 Mismatches 8;
 1ndels 0;
 Gaps 0;

 Qy
 1 DIOWINGSPSSLSASVGDRVIITCRASQGIRNDLGWYQQXFGKAPKRLIYAASSLQSGVPS 60
 1ndels 1nde

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Search completed: April 25, 2007, 04:08:29 Job time : 14.4506 secs

166, App 18, Appl 36, Appl 52, Appl 307, App 307, App 52, Appl 52, Appl 52, Appl 52, Appl 60, Appl

Sequence Sequence ( Sequence

Title: Perfect score:

Seguence:

OM protein

Run on:

Scoring table:

Searched:

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1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-041-860-22

| Sequence 22, Application US/10041860
| Publication No. US20030157109A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F. |
| APPLICANT: Corvalan, Jose R.F. |
| APPLICANT: Yang, Xiao-Chi |
| APPLICANT: Yang, Xiao-Dong |
| APPLICANT: Yang, Xiao-Dong |
| APPLICANT: Gazit, Gadi |
| APPLICANT: Gazit, Gadi |
| APPLICANT: Gazit, Gadi |
| APPLICANT: Bezabeh, Binyam |
| TITLE OF INVENTION: THEREOF |
| TITLE OF INVENTION: THEREOF |
| FILE REFERENCE: ABGENIX.051A |
| CURRENT APPLICATION NUMBER: US/10/041,860 |
| CURRENT FILING DATE: 2002-01-07 |
| NUMBER OF SEQ ID NOS: 377 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 22 |
| LENGTH: 107 |
| TYPE: PRT 
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                                              ALIGNMENTS
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Freg, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Prancine
APPLICANT: Gazit, Gadi
  107
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US-10-041-860-22
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RESULT 2
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                                                                                                                                                                              April 25, 2007, 04:18:18; Search time 40 Seconds (without alignments) 1251.741 Million cell updates/sec
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/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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558
1 DIQMIQSPSSLSASVGDRVT.......CLQHNSDPCSFGQGTKLEIR 107
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Sequence 2
Sequence 2
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                        GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-10-041-860-227

US-10-041-860-262

US-10-041-860-262

US-10-041-860-267

US-10-684-109-53

US-10-684-109-109

US-10-684-109-109

US-10-684-109-91

US-10-684-109-91

US-10-684-109-91

US-10-041-860-265

US-11-144-248-48

US-11-144-222-48

US-11-144-222-48

US-11-144-222-48

US-11-144-222-48

US-11-144-222-48

US-11-1860-26

US-10-330-613-18

US-10-041-860-28

US-10-041-860-28

US-10-041-860-231

US-10-041-860-231

US-10-041-860-231

US-10-041-860-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2097797 segs, 463214858 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Jia, Xiao-Chi
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                                                                                                                                                                                                                                                                                                                                                                   Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE REFERENCE: ABGENIX.051A
CURRENT APPLICATION: THRREOF
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
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                 APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 227
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 558; DB 4;
100.0%; Pred. No. 1.3e-40;
tive 0; Mismatches 0;
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Pred. No. 1.3e-40;
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100.0%; Pred. No. 1...
0; Mismatches
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RENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F.
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Best Local Similarity 100.
Matches 107; Conservative
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Best Local Similarity 100.
Matches 107; Conservative
  Weber, Richard
                                                                                                                                                                                                                                                                                      ; ORGANISM: homo sapiens
US-10-041-860-227
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US-10-041-860-262
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1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 558; DB 4; Length 107; 100.0%; Pred. No. 1.3e-40; tive 0; Mismatches 0; Indels (
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APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TILLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TILLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: 105/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S: 377
LENGTH: 107
                                              APPLICANT: "Local, Kichard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGRNIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0
Best Local Similarity 100.0
Matches 107; Conservative
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Best Local Similarity 100.0
Matches 107; Conservative
Yang, Xiao-Dong
                    Francine
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-262
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CORGANISM: homo sapiens
US-10-041-860-297
                          Chen,
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9 RESULT

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IS-10-684-109-109
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                                                                                                                            APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: LaRochelle, William
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WETHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: WISNG ANTI-PDGF-DD ANTIBODIES
TITLE OF INVENTION: OSLA
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US/10/665,383
CURRENT FILING DATE: 2003-09-16
PRIOR PELNG DATE: 2002-09-16
PRIOR PELNG DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 107
TYPE: PRT
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Sequence 5., Application US/10684109
Sequence 5. Application US/10684109
GENERAL INFORMATION:
APPLICANT: Devries, Peter J.
APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Reilly, Edward B.
APPLICANT: Reilly, Edward B.
TITLE OF INVENTION: Erythropoietin Receptor Binding
TITLE OF INVENTION: Antibodies
FILE REFERENCE: 6989 US. 02
CURRENT FILING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: 10/269,711
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR PILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 115
SOSTWARE: FREESE FREES FREES FREESE FREESE FREESE FREESE FREES FREESE FREESE FREESE FREESE FREESE FREESE FREES FREES
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Sequence 24, Application US/10665383; Publication No. US20040141969A1; GENERAL INFORMATION:
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LENGTH: 107
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21 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 80
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Pred. No. 6.5e-39;
2; Mismatches 1; Indels
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Pred. No. 5.5e-39;
3; Mismatches 1; Indels
                                                                         APPLICANT: Green, Larry L.
APPLICANT: Weilly, Edward B.
APPLICANT: Wieler, James
TITE OF INVENTION: Antibodies
TITE OF INVENTION: Antibodies
TILE OF INVENTION: Antibodies
TILE OF INVENTION: Antibodies
CURRENT APPLICATION NUMBER: US/10/684,109
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Getrow, David H.
APPLICANT: Reilly, Edward B.
APPLICANT: Wieler, James
TITLE OF INVENTION: Artibodies
TITLE OF INVENTION: Artibodies
FILE REFERENCE: 6989. US. 0.2
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR PILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4:
Sequence 109, Application US/10684109
Publication No. US20040175379A1
GENERAL INFORMATION:
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Publication No. US20040175379A1
GENERAL INFORMATION:
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Best Local Similarity 97.2%;
Matches 104; Conservative
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Best Local Similarity 96.3%;
Matches 103; Conservative
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; ORGANISM: Homo sapiens
US-10-684-109-109
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ORGANISM: Homo sapiens
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1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                         RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPCSFGGGTKLEIK 127
   61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
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; Sequence 265, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.;
; APPLICANT: Feng, Xiao-Chi
; APPLICANT: Chen, Xiao-Dong
; APPLICANT: Chen, Xiao-Dong
; APPLICANT: Chen, Xiao-Dong
; APPLICANT: Gazit, Gadi
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: ANTIBODIES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.011A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 3777
; SEQ ID NOS: 3777
; SEQ ID NO 265
; TENNEY FILING DATE: LENNEY FILE DATE SEASEROR FOR THE SECON TO 
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APPLICANT: Green, Larry L.
APPLICANT: Green, Larry L.
APPLICANT: Geren, Larry L.
APPLICANT: Geren, Larry L.
APPLICANT: Wieler, James
TITLE OF INVENTION: ETYThropoietin Receptor Binding
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION: Antibodies
TITLE OF INVENTION HUMBER: US/10/684,109
CURRENT APPLICATION NUMBER: 10/269,711
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FRASEQ EOF WINDOWS Version 4.0
                                                                                                                                                                                                                     US-10-684-109-91; Sequence 91, Application US/10684109; Publication No. US20040175379A1
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Matches 103; Conservative
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; ORGANISM: homo sapiens
US-10-041-860-265
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US-10-041-860-265
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Sequence 49, Application US/10/75444A

| Suguence 49, Application US/10/75444A
| Publication No. US2004020551A1
| GENERAL INFORMATION:
| APPLICANT: Cohen, Bruce D. |
| APPLICANT: Genez Andvarro, Jesus |
| APPLICANT: Obrocea, Mihail |
| APPLICANT: Page, Kelly L. |
| APPLICANT: Wang, Huifen F. |
| APPLICANT: Bage, Kelly L. |
| APPLICANT: Bage, Mariantin Ver. 2.1 |
| APPLICANT: Bage, Mariantin Ver. 2.1 |
| APPLICANT: Bage, Mariantin Ver. 2.1 |
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1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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APPLICANT: Cohen, Bruce D.
APPLICANT: Bebeb, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gorvalan, Jose R.
APPLICANT: GIANTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/10/038,591
CURRENT APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
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                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSDPCSFGQGTKLEIR 107
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94.6%; Score 528; DB 4; Length 236;
Best Local Similarity 95.3%; Pred. No. 1.1e-37;
Matches 102; Conservative 3; Mismatches 2; Indels
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Publication No. US20040086503A1
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APPLICANT: Beebe, Jean
APPLICANT: Beebe, Jean
APPLICANT: Beebe, Jean
APPLICANT: Miler, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TILLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PF2
CURRENT PAPLICATION NUMBER: US/11/144, 248
CURRENT PILING DATE: 2002-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                  23 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 82
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APPLICANT: Miler, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Moyer, James D.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REPERENCE: ABX-PPS.
CURRENT APPLICATION NUMBER: US/11/144,222
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
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Query Match

94.6%; Score 528; DB 4; Length 236;
Best Local Similarity 95.3%; Pred. No. 1.1e-37;
Matches 102; Conservative 3; Mismatches 2; Indels
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Publication No. US20050281812A1
; GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
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Best Local Similarity 95.3
Matches 102; Conservative
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US-11-144-248-48
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US-11-144-222-48
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61, Appl
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232, App
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Sequence 227, App
                                                                          April 25, 2007, 04:23:02 ; Search time 41 Seconds (without alignments) 533.620 Million cell updates/sec
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FEMC_CELETRA_SIDS3/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
FEMC_CELETRA_SIDS3/prodata/1/pubpaa/USO7_NEW_PUB.pep:*
FEMC_CELETRA_SIDS3/prodata/1/pubpaa/NEW_PUB.pep:*
FEMC_CELETRA_SIDS3/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
FEMC_CELETRA_SIDS3/prodata/1/pubpaa/USI0_NEW_PUB.pep:*
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1 DIQMTQSPSSLSASVGDRVT......CLQHNSDPCSFGQGTKLEIR 107
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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US-11-109-181-227

US-11-109-181-261

US-11-109-181-267

US-11-109-181-267

US-11-109-181-267

US-11-109-181-265

US-11-200-687-27

US-11-200-687-27

US-11-200-687-27

US-11-404-967-27

US-11-109-181-28

US-11-109-181-28

US-11-109-181-28

US-11-109-181-28

US-11-109-181-28

US-11-109-181-28

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US-11-109-181-268

US-11-109-181-268
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Maximum Match 100%
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                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 1
Sequence 2
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Sequence 2
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GENERAL INVERTION:
GENERAL INVERTION:
APPLICANT: Uia, Xiao-Chi
APPLICANT: Uia, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Peng, Xiao
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO COURTENT APPLICANTON THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: 2005-04-18
FRIOR APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
FRIOR FILING DATE: 2005-01-07
NUMBER OF SEQ ID NOS: 377
SEQ ID NO 2:
SEQ ID NO 2:
CERNOTH: 107
TITLE OF INVENTION TO THE COURTED TO THE 
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100.0%; Pred. No. 1.5e-44;
tive 0; Mismatches 0;
                                        US-11-311-939-9

US-11-311-939-181

US-11-311-939-181

US-11-331-939-113

US-11-311-939-113

US-11-311-939-1149

US-11-290-687-20

US-11-290-687-20

US-11-404-967-28

US-11-404-967-28

US-11-109-181-18

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285

US-11-109-181-285
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Publication No. US20060293506A1
GENERAL INFORMATION:
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                                             , ORGANISM: homo sapiens
US-11-109-181-22
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Best Local Similarity
Matches 107; Conserv
61
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Sequence 227, Application US/11109181; Publication No. US20060293506A1; GENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi

Sequence Sequence

Sequence

US-11-109-181-227

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i Sequence 261, Application US/11109181

i Sequence 261, Application US/11109181

i Publication No. 202060293506A1

i GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Yang, Xiao-Chi

APPLICANT: Tang, Xiao-Dong

APPLICANT: Gazit, Gadi

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION UNMERR: US/11/109,181

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US/10/041,860

PRIOR FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH 107
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gaber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 3002-01-07
NUMBER OF SEQ ID NOS: 377
SOTTWARE: FRASEC for Windows Version 4.0
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100.0%; Score 55%; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0;
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Best Local Similarity 100.'
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homo sapiens
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LENGTH: 107
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1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
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Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels (
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                                                                                                                           APPLICANT: Peng, Xiao
APPLICANT: Peng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gal
APPLICANT: Gazit, Gal
APPLICANT: Gazit, Gal
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 107
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APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
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CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
FRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 107
TYPE: PRT
Sequence 262, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
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CORGANISM: homo sapiens
US-11-109-181-262
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US-11-109-181-297
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Best Local Similarity
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US-11-109-181-265
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| Sequence 384, Application No. US20060286112A1
| GENERAL INFORMATION:
| APPLICANT: Relarman, Sirid-Aimee
| APPLICANT: Relouski, Shelley Sims
| APPLICANT: Belouski, Shelley Sims
| APPLICANT: Belouski, Shelley Sims
| APPLICANT: Belouski, Shelley Sims
| APPLICANT: Green, Larry Lar
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Publication No US20060286112A1
GENERAL INFORMATION:
APPLICANT: Rellermann, Sirid-Aimee
APPLICANT: Bebucki, Shelley Sims
APPLICANT: Bebucki, Shelley Sims
APPLICANT: Green, Larry L.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
TITLE OF INVENTION: OTHER DISORDERS
FILE REFERENCE: ABENIX.120A
CURRENT APPLICATION NUMBER: US/11/433,924
CURRENT FILING DATE: 2006-05-12
PRIOR APPLICATION NUMBER: US 60/681,846
PRIOR FILING DATE: 2006-05-16
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    0; Indels
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    Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 376
LENGTH: 107
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Matches 104; Conservative
107; Conservative
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ORGANISM: Homo sapiens
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US-11-433-924-376
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US-11-433-924-384
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US-11-433-924-376
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Matches
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1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLQSGVPS 60
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FUBLICANT: COLVAIAN.

GENERAL INFORMATION:

APPLICANT: COLVAIAN, JOSE R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Dong

APPLICANT: Feng, Xiao-Dong

APPLICANT: Feng, Xiao-Dong

APPLICANT: Gazit, Gadi

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber,
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Pred. No. 9.2e-42;
3; Mismatches 2; Indels
                                                                             1; Indels
Score 535; DB 7;
Pred. No. 2.1e-42;
                                                                         4; Mismatches
95.9%;
ilarity 95.3%;
Conservative
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Best Local Similarity 95.3%;
Matches 102; Conservative
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ORGANISM: homo sapiens
   Query Match
Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                            Score 528; DB 6; Length 108;
Pred. No. 9.3e-42;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoet, Rene
APPLICANT: Schoonbroodt, Sonia
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: LIBRARIES AND METHODS FOR
TITLE OF INVENTION: LISCATING ANTIBODIES
FILE REFERENCE: 10280-116001
CURRENT FILING DATE: 2006-02-01
PRIOR PELLING DATE: 2006-02-01
PRIOR FILING DATE: 2005-02-01
                                                                                                                                                                                                                     ; OTHER INFORMATION: human V-L germline sequence US-10-515-149-39
PRIOR APPLICATION NUMBER: US 60/390,033
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: WO PCT/US03/19333
PRIOR FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 39
LENGTH: 108
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 108
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; Sequence 61, Application US/11346403A
; Publication No. US20060234302A1
                                                                                                                                                                                                                                                                                 94.6%;
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ORGANISM: Artificial Sequénce
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Best Local Similarity
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Sequence 27, Application US/11290687 Publication No. US20060140960A1 GENERAL INFORMATION:

APPLICANT: Wang, Yan APPLICANT: Pachter, Jonathan APPLICANT: Wang, Yaolin

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Page 4

APPLICANT: Liu, Ming
TITLE OF INVENTION: BIOMARKERS FOR PRE-SELECTION OF PATIENTS FOR ANTI-IGFIR THERAPY
FILE REFERENCE: JB06257 US01
CURRENT APPLICATION NUMBER: US/11/290,687
CURRENT FILING DATE: 2005-11-30
PRIOR APPLICATION NUMBER: 60/633,156
PRIOR PRILING DATE: 2004-12-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
LEMOTH: 236
TYPE: LEMOTH: 236
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APPLICANT: Wang, Yan
APPLICANT: Pachter, Jonathan A
APPLICANT: Bishop, Walter R
TITLE OF INVENTION: Methods and Compositions for Treating or Preventing Cancer
FILE REFERENCE: OCO6331 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
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Pred. No. 2.1e-41;
3; Mismatches 2;
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CURRENT FILING DATE: 2006-04-14
PRIOR APPLICATION NUMBER: 60/671,654
PRIOR FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.3
SEQ ID NO 27
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/11404967
Publication No. US20060233810A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.6%;
Best Local Similarity 95.3%;
Matches 102; Conservative
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US-11-239-308-8
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              APPLICANT: Smider, Vaughn
APPLICANT: Smider, Vaughn
APPLICANT: Larrick, James W.
APPLICANT: Larrick, James W.
APPLICANT: Integrigen, Inc.
TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
FILE REFERENCE: 021216-0003100S
CURRENT APPLICATION NUMBER: US/11/239,308
CURRENT APPLICATION NUMBER: US/10/683,733
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 2003-10-09
PRIOR FILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
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Pred. No. 1.8e-41;
4; Mismatches 2; Indels
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Sequence 18, Application US/11479339

Bulication No. USZO060246077A1

GENERAL INFORMATION:
APPLICANT: Menashe, Bar-Eli
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN
FILE REPRENCE: AGGENTX: 0300.2

CURRENT APPLICATION NUMBER: US/11/479,339

CURRENT FILING DATE: 2006-06-30

PRIOR APPLICATION NUMBER: 10/660,357

PRIOR PILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 18

LENGTH: 107
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94.4%;
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Best Local Similarity 94.4'
Matches 101; Conservative
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Matches 101, Conservative
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; ORGANISM: Homo sapiens
US-11-239-308-8
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; ORGANISM: Homo Sapiens
US-11-479-339-18
GENERAL INFORMATION:
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 525; DB 7; Length 107; Pred. No. 1.8e-41; 4; Mismatches 2; Indels
                                                                                                                               APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT PILING DATE: 2002-04-18
FRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
Sequence 26, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
                                                                               APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapiens
US-11-109-181-26
                                                                                                           APPLICANT:
APPLICANT:
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Search completed: April 25, 2007, 04:27:43 Job time: 41.2585 secs

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6.2.1
Biocceleration Ltd.
version (
 GenCore
Copyright (c) 1993
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protein search, using sw model OM protein -

April 25, 2007, 03:54:56 ; Search time 112 Seconds (without alignments) 564.248 Million cell updates/sec Run on:

1 EVQLVQSGAEVKKPGESLKI.......YYYYHGMDVWGQGTTVTVSS US-10-665-383-38 score:

129

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

Title: Perfect

2782304 segs, 489333398 residues Searched:

2782304 Potal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A\_Geneseq\_200701:\* 1: genesecn1940:.. Database :

geneseqp2003bs:\* geneseqp2003ав:\* geneseqp2007s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp20048:\* geneseqp2005s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES Re

Description	Adk18605 Anti-huma	Adk18791 Anti-huma	Adk18895 Anti-huma	Adk18826 Anti-huma	Adl25428 Human mAb	Aea12652 Heavy cha	Aea12653 Heavy cha	Aeal8909 Variant h	Aea18908 Heavy cha	Aea18548 Heavy cha	Aea18549 Variant o	Aeal0642 Human ant	Aeal0641 Human ant	Aed25714 Monoclona	Aed25715 Monoclona	Aed24416 Human CHI	Aed24415 Human CHI	Aed25981 Ant-CD40	Aed25980 Ant-CD40	Ady26764 Anti-NGF-	Adk18889 Anti-huma	Adk18603 Anti-huma
ID	ADK18605	ADK18791	ADK18895	ADK18826	ADL25428	AEA12652	AEA12653	AEA18909	AEA18908	AEA18548	AEA18549	AEA10642	AEA10641	AED25714.	AED25715	AED24416	AED24415	AED25981	AED25980	ADY26764	ADK18889	ADK18603
DB	.7	7	7	7	80	σ	σ	σ	σ	σ	δ	σ	σ	σ	σ	σ	σ	σ	σ	σ	7	7
Length	129	129	129	129	129	474	474	474	474	474	474	474	474	474	474	474	474	474	474	125	126	126
% Query Match	100.0	100.0	100.0	100.0	100.0	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	86.3	85.6	84.9
Score	669	669	669	669	669	623	623	623	623	623	623	623	623	623	623	623	623	623	623	603	598.5	593.5
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Adk18790 Anti-huma Adk18825 Anti-huma Ad125424 Human mAb Adk18876 Anti-huma Adk18599 Anti-huma Adk18824 Anti-huma Ad125416 Human mAb Ad125416 Human nAb	Aek98296 Human 161 Aek9821 Human 161 Aek98278 Human 161 Adp47228 Human pho Aek98274 Human 161	w	Ad125440 Human mAb Adp47088 Human pho Adp47224 Human pho Adp47225 Human pho Adp47098 Human pho
7 ADK18790 7 ADK18825 8 ADL25424 7 ADK18876 7 ADK18599 7 ADK18599 8 ADL25416 10 AEK98291	10 AEK98296 10 AEK98221 10 AEK98278 8 ADP47228 10 AEK98274	10 AEK98213 7 ADK18827 7 ADK18611 7 ADK18792 7 ADK18913	8 ADL25440 8 ADP47088 8 ADP47224 8 ADP47225 8 ADP47098
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22 22 23 23 26 26 27	33 3 3 3 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5	333 433 40 40 40	4 4 4 4 4 4 4 6 4 7

### ALIGNMENTS

antiinflammatory; immunomodulator; cytostatic; gene therapy Anti-human PDGF-D antibody heavy chain protein sequence. ADK18605 standard; protein; 129 AA. (first entry) sapiens. 06-MAY-2004 ADK18605; Ношо RESULT 1 ADK18605 

WO2003057857-A2. 17-JUL-2003.

06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860.

(ABGE-) ABGENIX INC.

Weber R; Gazit G, Chen F, Yang X, Feng X, Corvalan JRF, Jia X, Bezabeh B;

WPI; 2003-587119/55.

growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 29; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for stading various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.

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120
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                            Length 129;
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                           Score 699; DB 7;
Pred. No. 5.2e-56;
                                                       Mismatches
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                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                                                                                                                                                                                            ADK18895 standard; protein; 129
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hes 129; Conserv
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121 OGTTVTVSS 129

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1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY

100.0%; Score 699; DB 7; Length 129; 100.0%; Pred. No. 5.2e-56; tive 0; Mismatches 0; Indels

Matches 129; Conservative

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Best Local Similarity

Query Match

antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; antibhritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antifinamatory; dermatological; immunosuppressive; antidiabetic;

gene therapy; human; monoclonal antibody; mAb

Human mAb 1.29 heavy chain variable region protein SEQ ID NO:38

17-JUN-2004 (first entry)

ADL25428;

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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for recating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                  Weber R;
                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibody that binds to platelet-derived
                                                                                                                                                                                                                                                                                                                                                            factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                                                                                                                                 antiinflammatory; immunomodulator; cytostatic; gene therapy
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100.0%; Pred. No. 5.2e-56;
ive 0; Mismatches 0;
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                                                             ADK18826 standard; protein; 129 AA
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||||||||||||||||||||||QGTTVTVSS 129
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           121
                                                                                   ADK18826;
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                                                    ADK18826
           셤
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present invention describes an antibody or its binding fragment that

Disclosure; SEQ ID NO 38; 115pp; English.

nephritis

Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating

Larochelle WJ, Lichenstein H;

Keyt B,

Floege J, Gazit-Bornstein G,

WPI; 2004-269881/25. N-PSDB; ADL25427.

(ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.

16-SEP-2003; 2003WO-US029414. 16-SEP-2002; 2002US-0411137P

WO2004024098-A2 sapiens.

Ношо

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binds plated the derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

(1) a method of detecting nephritis; (2) a method of treating nephritis;
of treating mesangial cell proliferation; and (4) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulomephritis. The antibody has nephrotropic, antihilammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulomephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSFQCQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
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Matches 129; Conservative
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AEA12652
ID AEA1
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Indels

Matches 129; Conservative

Local Similarity

9 9 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120 SPSFQCQATISADXSISTAYLOWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120

ADL25428 standard; protein; 129 AA.

RESULT 5
ADL25428
ID ADL2:

129

QGTTVTVSS

QCTTVTVSS 129

121 121

8

61 61

1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY

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(first entry)

sapiens.

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cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic; b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain;
                                 Heavy chain variant of CHIR-5.9 human anti-CD40 antibody.
                                                                                                                                                                                                                         04-NOV-2003; 2003US-0517337P.
26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565710P.
28-SEP-2004; 2004US-0613885P.
                                                                                                                                                                                                  04-NOV-2004; 2004WO-US037159.
                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP
                                                                                                                                                 WO2005044307-A2.
           28-JUL-2005
                                                                                                                                                                         19-MAY-2005
                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                               Long L,
                                                                                    mutein.
                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for treating a human subject for a cancer characterized by neoplastic B cell growth. The method comprises administering to the subject combination antibody therapy, which comprises an amount of an anti-CD40 antibody or its antigen-binding fragment in combination with an anti-CD40 antibody or its antigen-binding fragment, where the anti-CD40 antibody or antigen-binding fragment is gonist activity when bound to the CD40 antigen. The invention further comprises: methods of inhibiting the growth of a tumor comprising neoplastic B cells. The methods and compositions have cytostatic activity. The methods are useful for treating B cell-related cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for the treatment of such a disease. This sequence represents a heavy chain
                                                                                                                                                                                                                                                                                                                                                    Treating human subjects for B cell-related cancers (e.g. multiple myeloma or Burkitt's lymphoma) comprises administering to the subject an amount of an antagonist anti-CD40 antibody in combination with an anti-CD20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                       cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic; b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 623; DB 9; Length 474;
Pred. No. 1.8e-48;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of CHIR-5.9 human anti-CD40 antibody of the invention
                                                 of CHIR-5.9 human anti-CD40 antibody.
                                                                                                                                                                                                                                                                                                      Yabannavar A, Zaror I;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 7; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%;
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26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565710P.
28-SEP-2004; 2004US-0613885P.
                                                                                                                                                                                       04-NOV-2004; 2004WO-US037159
                        (first entry)
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Best Local Similarity 91.5<sup>3</sup>
Matches 118, Conservative
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                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                               WPI; 2005-346957/35
                                                                                                                                                                                                                                                                                                      Lugman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 474 AA;
                                                                                                                                      WO2005044307-A2
                                                                                                                Homo sapiens
                       28-JUL-2005
                                                 Heavy chain
                                                                                                                                                              19-MAY-2005
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Zaror I;

Yabannavar A,

Luqman M,

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The invention relates to a novel method for treating a human subject for a cancer characterized by neoplastic B cell growth. The method comprises administering to the subject combination antibody therapy, which comprises an amount of an anti-CD40 antibody or its antigen-binding fragment in combination with an anti-CD20 antibody or its antigen-binding fragment, where the anti-CD40 antibody or antigen-binding fragment, where the anti-CD40 antibody or antigen-binding fragment is free of significant agonist activity when bound to the CD40 antigen. The invention further comprises: methods of inhibiting the growth of a tumor comprising neoplastic B cells. The methods and compositions have cytostatic activity. The methods are useful for treating B cell-related cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for the treatment of such a disease. This sequence represents a heavy chain variant of a CHIR-5.9 human anti-CD40 antibody of the invention.
                                                          Treating human subjects for B cell-related cancers (e.g. multiple myeloma or Burkitt's lymphoma) comprises administering to the subject an amount of an antagonist anti-CD40 antibody in combination with an anti-CD20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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Best Local Similarity 91.5%; Pred. No. 1.8e-48;
Matches 118; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 8; 133pp; English.
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WPI; 2005-346957/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 474 AA;
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AEA18909
ID AEA1
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AEA12653 standard; protein; 474 AA.

RESULT 7 **AEA12653**  AEA12653;

CLL; anti-CD40 antibody; CD40; CHIR-5.9;

Heavy chain of CHIR-5.9 human anti-CD40 antibody.

CHIR-12.12; antibody therapy; heavy chain

Synthetic

Peptide

chronic lymphocytic leukemia;

/note= "variable region" 145. .474 /note= "constant region"

20. 144

Region legion

/note= "leader peptide"

Location/Qualifiers

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The specification describes a method of treating a human subject for chronic lymphocytic leukemia (CLL). The method comprises administering an amount of a human anti-CD40 monoclonal antibody that specifically binds to a human CD40 antiqen expressed on the surface of a human CD40-expressing cell and is free of significant agonist activity, where when the antibody binds to the CD40 antigen expressed on the surface of the cell, the growth or differentiation of the cell is inhibited. The human anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12. The method of the invention is useful for treating chronic lymphocytic leukemia or in manufacturing medicaments for the treatment of such anti-CD40 monoclonal antibody CHIR-5.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating human subjects for chronic lymphocytic leukemia comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen.
                                                                                                   chronic lymphocytic leukemia; CLL; anti-CD40 antibody; CD40; CHIR-5.9; CHIR-12.12; antibody therapy; heavy chain.
                                                                   Jariant heavy chain of CHIR-5.9 human anti-CD40 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                    Aukerman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 8; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  Lugman M, Yabannavar A,
                                                                                                                                                                                                                                                                                                             26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565710P.
21-SEP-2004; 2004US-0611794P.
                                                                                                                                                                                                                                                            04-NOV-2004; 2004WO-US036954
                                                                                                                                                                                                                                                                                               2003US-0517337P
                                 (first entry)
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                                                                                                                                                                                                                                                                                            04-NOV-2003;
26-NOV-2003;
                                 28-JUL-2005
                                                                                                                                                                                                                            19-MAY-2005
                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 Long L,
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administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen.

Claim 1; SEQ ID NO 7; 115pp; English

Treating human subjects for chronic lymphocytic leukemia comprises

Aukerman L;

Zaror I,

Yabannavar A,

WPI; 2005-346955/35. Long L, Luqman M,

04-NOV-2003; 2003US-0517337P. 26-NOV-2003; 2003US-052559P. 27-ARR-2004; 2004US-0565710P. 21-SEP-2004; 2004US-0611794P.

(CHIR ) CHIRON CORP.

04-NOV-2004; 2004WO-US036954

WO2005044304-A2

19-MAY-2005

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SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                     80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR----GTAAGRDYYYYYGMDVWG 135
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                                                                                               20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                       EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                       Gaps
                                         4,
Query Match 89.1%; Score 623; DB 9; Length 474; Best Local Similarity 91.5%; Pred. No. 1.8e-48; Matches 118; Conservative 1; Mismatches 6; Indels
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The specification describes a method of treating a human subject for chronic lymphocytic leukemia (CLL). The method comprises administering an amount of a human anti-CD40 monoclonal antibody that specifically binds to a human CD40 antigen expressed on the surface of a human CD40-expressing cell and is free of significant agonist activity, where when the antibody binds to the CD40 antigen expressed on the surface of the cell, the growth or differentiation of the cell is inhibited. The human anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12. The method of the invention is useful for treating chronic lymphocytic leukemia or in manufacturing medicaments for the treatment of such cliseases. The present sequence represents the heavy chain of human anti-CD40 monoclonal antibody CHIR-5.9.
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Pred. No. 1.8e-48;
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91.5%;
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Matches 118, Conservative
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RESULT 10 AEA18548

AEA18908 standard; protein; 474 AA

RESULT 9 **AEA**18908 (first entry)

28-JUL-2005

AEA18908;

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     solid tumor comprising carcinoma cells expressing C140 antigen. The method comprises administering to the subject an amount of a human anti-CD40 monoclonal antibody that is capable of specifically binding to the CD40 antigen, the monoclonal antibody being free of significant agonist activity when bound to CD40 antigen. The method of the invention is useful for treating solid tumors expressing the CD40 cell-surface antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary, skin, colon or urinary bladder, or in manufacturing medicaments for the treatment of such diseases. The present sequence represents the heavy chain of anti-CD40 monoclonal antibody CHIR-5.9. This antibody represents an antibody which can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification describes a method of treating a human subject for a
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                                                                                        cytostatic; gene therapy; neoplasm; solid tumor; CD40; heavy chain; antibody CHIR-5.9; antibody therapy; ss.
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                                                                  Heavy chain of anti-CD40 antibody CHIR-5.9
                                                                                                                                                                                                                      "constant region"
                                                                                                                                                               . .19
'note= "leader peptide"
                                                                                                                                                                                               /note= "variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 7; 123pp; English
                                                                                                                                                   cocation/Qualifiers
AEA18548 standard; protein; 474 AA
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26-NOV-2003; 2003US-052579P.
27-ARR-2004; 2004US-056634P.
27-ARR-2004; 2004US-0565710P.
                                                                                                                                                                                                                                                                                           04-NOV-2004; 2004WO-US036955
                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-346956/35.
                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 474 AA;
                                                                                                                                                                                                                                             WO2005044305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen.
                                             28-JUL-2005
                                                                                                                                                                                                                                                                    19-MAY-2005
                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                  Long L,
                                                                                                                                                          Peptide
                                                                                                                                                                                    Region
                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD40
                                                                                                                                                    Key
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121 QGTTVTVSS 129

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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a method of treating a human subject for a solid tumor comprising carcinoma cells expressing CD40 antigen. The method comprises administering to the subject an amount of a human anti-CD40 monoclonal antibody that is capable of specifically binding to the cD40 antigen, the monoclonal antibody being free of significant agonist activity when bound to CD40 antigen. The method of the invention is useful for treating solid tumors expressing the CD40 cell-surface antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary, skin, colon or urinary bladder, or in manufacturing medicaments for the treatment of such diseases. The present sequence represents a variant of the heavy chain of anti-CD40 monoclonal antibody CHIR-5.9, comprising a ser for Ala substitution at site 158. This antibody represents an antibody which can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating human subjects for solid tumors that express CD40 cell-surface. antigen comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EVQLVQSGABVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; neoplasm; solid tumor; CD40; heavy chain; antibody CHIR-5.9; antibody therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                        Variant of the heavy chain of anti-CD40 antibody CHIR-5.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%; Score 623; DB 9;
91.5%; Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zaror I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 8; 123pp; English.
                                                                                                                                                              AEA18549 standard; protein; 474 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565634P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-2004; 2004US-0565710P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 OGTTVTVSS 129
136 QGTTVTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-346956/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luqman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2005044305-A2.
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                                                                                                                                                                                                                                                                                           28-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                              AEA18549;
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79

Gaps

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Indels

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04-NOV-2003; 2003US-0517337B.
26-NOV-2003; 2003US-0525579P.
26-APR-2004; 2004US-0565709P.
27-APR-2004; 2004US-0565710P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-2004; 2004WO-US037281
136 QGTTVTVSS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-347055/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2005044855-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                   28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chain.
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                                                                                                                                                                                            AEA10642;
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Region
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYYHGMDVWG 120
                                                                                                                                             80 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR----GTAAGRDYYYYYGMDVWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple myeloma; hematological disease; immune disorder; antibody; antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;
                                                                            20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVROMPGKGLEWMGIIYPGDSDTRY
                                       EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "A variant exists in which wild-type Ala may
substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human anti-CD40 monoclonal antibody 5.9 heavy chain protein.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l. .19
'note= "Leader region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              AEA10641 standard; protein; 474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yabannavar A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-2003; 2003US-0517337P.
26-NOV-2003; 2003US-052579P.
26-APR-2004; 2004US-0565709P.
27-APR-2004; 2004US-0565710P.
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                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2005 (first entry)
  118; Conservative
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                                                                                                                                                                                                     129
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                                                                                                                                                                                                     121 QGTTVTVSS
                                                                                                                                                                                                                                          OGTTVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2005044855-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain
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                                                                                                                                                                                                                                            136
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                                                                                                                                                                                                                                                                                                      RESULT 13
AEA10641
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple myeloma comprising administering to the subject an amount of a human anti-CD40 monoclonal antibody that specifically binds to a human CD40 antigen expressed on the surface of a human CD40-expressing cell and that is free of significant agonist activity, where the binding of the antibody to the CD40 antigen expressed on the surface of the cell and in inhibition of the growth or differentiation of the cell. Multiple myeloma is a B-cell malignancy characterized by latent accumulation of secretory plasma cells in the bone marrow, these cells having a low proliferative index and an extended life span. The disease ultimately attacks bones and bone marrow, resulting in multiple tumors and legions throughout the skeletal system. The method of the invention demonstrates cytostatic and gene therapy applications and may be useful for treating multiple myeloma or in manufacturing medicaments for the treatment of such a disease. The current sequence is that of the human anti-CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating human subjects for multiple myeloma comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for treating a human subject for
                                                                                                                                                                                                                                                             multiple myeloma; hematological disease; immune disorder;
antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9 heavy chain variant protein of the invention
                                                                                                                                                                                                                       Human anti-CD40 monoclonal antibody 5.9 heavy chain variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild-type Ala has been substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zaror I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Constant region"
                                                                                                                                                                                                                                                                                                                                                                                                        1. .19
/note= "Leader region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 8; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                               AEA10642 standard; protein; 474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Long L, Luqman M, Yabannavar A,
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .474
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The invention relates to a novel method for treating a human subject for multiple myeloma comprising administering to the subject an amount of a human anti-CD40 monoclonal antibody that specifically binds to a human CD40 antigen expressed on the surface of a human CD40-expressing cell and that is free of significant agonist activity, where the binding of the antibody to the CD40 antigen expressed on the surface of the cell results in inhibition of the growth or differentiation of the cell. Multiple myeloma is a B-cell malignancy characterized by latent accumulation of Treating human subjects for multiple myeloma comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen. Zaror Claim 1; SEQ ID NO 7; 115pp; English.

Score 623; DB 9; Length 474; Pred. No. 1.8e-48;

89.1**%**; 91.5**%**;

Best Local Similarity

Query Match

Sequence 474 AA;

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SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPSFQGQVIISADKSISTAYLQWSSLKASDTAMYYCAR----GTAAGRDYYYYYGMDVWG 135
                       proliferative index and an extended life span. The disease ultimately statacks bones and bone marrow, resulting in multiple tumors and legions throughout the skeletal system. The method of the invention demonstrates cytostatic and gene therapy applications and may be useful for treating multiple myeloma or in manufacturing medicaments for the treatment of such a disease. The current sequence is that of the human anti-CD40 monoclonal antibody 5.9 heavy chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20. .474 _____/note= "Mature monoclonal anti-CD40-antibody CHIR-5.9
                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; monoclonal antibody; antibody therapy; cancer; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy
secretory plasma cells in the bone marrow, these cells having a low
                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                           Length 474;
                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hurst D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain.
                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                           Score 623; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zaror I,
                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain constant region"
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                                                                                                                                                                                                                                                                                                           89.1%;
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26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565710P.
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Menezes DE;
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                      Sequence 474 AA;
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The invention describes a method of treating (M1) a human subject for cancer comprising neoplastic cells expressing CD40 antigen. The method control involves administering to the subject, a combination therapy including administration of an anti-CD40 antibody in combination with an interleukin-2 (IL-2), where the anti-CD40 antibody is the monoclonal antibody CHIR-2.9 or CHIR-12.12. (M1) is useful for treating a human subject for cancer comprising neoplastic cells expressing CD40 antigon, where the cancer is a B cell-related cancer or solid tumor. The B cell-control cancer is chosen from non-Hodgkin's lymphoma, chronic lymphocytic leukemia, multiple myeloma, B cell lymphoma, high-grade B cell lymphoma, intermediate-grade B cell lymphoma, high-grade B cell lymphoma, control lymphoma, high-grade B cell lymphoma, high-grade B cell lymphoma, control lymphoma, follicular large cell lymphoma, high-grade B cell lymphoma, control lymphoma, follicular small cleaved lymphoma, control lymphocytic leukemia, lymphoma, microal large cell lymphoma, diffuse small cleaved lymphoma, control lymphoma, mucosal associated lymphoma diffuse large cell lymphoma, machonial large B cell lymphoma, lymphoma, mocosal associated lymphoma, lymphoma, microblastic large cell lymphoma, lymphoma, microblastic lymphoma, lymphoma, lymphoma, diffuse large cell lymphoma and mantle cell lymphoma, lymphoma, lymphoma, microblastic carcinoma, lymphoma, lymphoma, nasopharyngeal colon carcinoma, prostate cancer, renal cell carcinoma, colon carcinoma, prostate cancer, renal cell carcinoma, calinoma, lymphoma, carcinoma, calinoma, lymphoma, carcinoma, carcinoma, lung carcinoma, cell carcinoma, cell carcinoma, cell carcinoma, lung cell carcinoma, cell carc
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Treating human subject for cancer comprising neoplastic cells expressing
               CD40 antigen, by administering combination therapy including administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with interleukin-2, to subject.
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Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
89.1%; Score 623; DB
Best Local Similarity 91.5%; Pred. No. 1.8e
Matches 118; Conservative 1; Mismatches
                                                                                                                         Claim 1; SEQ ID NO 7; 204pp; English
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cancer comparising to the subject, a combination with an enthod involves administering to the subject, a combination with an administration of an anti-CD40 antibody in combination with an inti-CD40 antibody is the monoclonal antibody CHIR-5.9 or CHIR-12.12. (MI) is useful for treating a human subject for cancer comprising neoplastic cells expressing CD40 antigen, where the cancer comprising neoplastic cells expressing CD40 antigen, where the cancer comprising neoplastic cells expressing CD40 antigen, where the cancer is a B cell-related cancer or solid tumor. The B cell-related sell-spends B cell lymphoma, high-grade B cell lymphoma, intermediate-grade B cell lymphoma, intermediate-grade B cell lymphoma, molosolastic leukemia, myelolastic leukemia, Hodgkin's disease, plasmacytoma, follicular lymphoma, follicular mixed small cleaved lymphoma, cellicular mixed small cleaved lymphoma, diffuse small lymphoma, mucosal associated lymphoma, diffuse small lymphoma, splenic lymphoma, harry cell leukemia, diffuse large cell lymphoma, mucosal associated lymphoma, lymphoma, marginal account lymphoma, manual large B cell lymphoma, myentong granulomatosis, diffuse mixed cell lymphoma, mediastinal large B cell lymphoma, lymphoma, mucosal associated lymphoma, lymphoma, molosolastic lymphoma, lymphoma, molosolastic lymphoma, lymphoma, molosolastic lymphoma, lymphoma, diffuse large cell lymphoma immunoblastic lymphoma, lymphoma, mucosal sarcinoma, breast carcinoma, breast carcinoma, gastric carcinoma, presstre carcinoma, neolia carcinoma, presste carcinoma, liver carcinoma, associate carcinoma, liver carcinoma, associate carcinoma, liver carcinoma, associate carcinoma, liver carcinoma, neolia carcinoma, presste carcinoma, liver carcinoma, neolia carcinoma, presste carcinoma, liver carcinoma, mascopharyngeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating human subject for cancer comprising neoplastic cells expressing CD40 antiden, by administering combination therapy including administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with interleukin-2, to subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma, squamous cell carcinoma, thyroid papillary carcinoma, melanoma, ovarian carcinoma, lung carcinoma, cervical carcinoma and sarcomas. This is the amino acid sequence of human monoclonal anti-CD40-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of treating (M1) a human subject for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 8; 204pp; English.
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                                                                                                                         04-NOV-2004; 2004WO-US036958.
                                                                                                                                                                                     04-NOV-2003; 2003US-0517337P.
26-NOV-2003; 2003US-0525579P.
27-APR-2004; 2004US-0565710P.
                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                            Long L, Luqman M,
Lopes De Menezes DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-746884/76.
                         WO2005044294-A2.
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                                                                               19-MAY-2005.
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Zaror I,

4; Gaps 89.1%; Score 623; DB 9; Length 474; 91.5%; Pred. No. 1.8e-48; ive 1; Mismatches 6; Indels Best Local Similarity 91.5 Matches 118; Conservative Query Match ò

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OGTIVIVSS 129 121

136 QGTTVTVSS 144

Search completed: April 25, 2007, 04:05:19 Job time : 111.873 secs

us-10-665-383-38.rpr

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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 04:05:37 ; Search time 10 Seconds (without alignments) 1261.509 Million cell updates/sec

US-10-665-383-38 699 1 EVQLVQSGAEVKKPGESLKI......YYYYHGMDVWGQGTTVTVSS 129 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heavy chain V	g heavy chain V	q heavy chain -	heavy	g heavy chain V	6	g heavy chain V	g heavy	g heavy chain V	g heavy chain V	g heavy chain V	g heavy	g heavy chain V	d heavy chain V	g heavy														
SUMMARIES	ID	A49047	PH1422	PH1558	C36006	PH1428	S38492	PH1563	PH1414	S31685	PH1561	PH1423	PH1415	PH1559	PH1420	PH1419	PH1565	PH1417	PH1418	PH1416	819670	PH1413	PH1424	S16685	PH1564	PH1411	S26907	4	PH1279	ŝ
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	Length	136	134	139	123	113	123	144	127	141	147	123	127	136	127	126	138	126	126	126	117	123	126	128	138	127	86	101	102	115
d	Query Match	87.2	84.0	82.5	82.1	80.7	80.3	80.3	79.8	79.2	79.0	78.3	78.1	78.1	78.0	77.6	77.1	76.8	76.8	75.8	75.7	75.5	75.5	75.4	74.8	74.5	74.2	74.2	74.2	74.2
	Score	0	587.5	-	574	564	561	561	558	553.5	L)	547	546	546		542.5		536.5	ന	N	529		527.5	527	523	521	519	519	519	519
	Result No.	Н	7	ю	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

115 GMDVWGQGTTVTVSS 129 ||||||:|||||||| 122 GMDVWGEGTTVTVSS 136

ò g RESULT 2
PH1422
CJ Decay Chain V region (clone P3-69) - human (fragment)
CJ Decay Chain V region (clone P3-69) - human (fragment)
CJ Decay Chain V region (clone P3-69) - human (fragment)
CJ Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000
CJ Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000
CJ Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000
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30         517         74.0         119         2         S36257         Ig heavy chain V r r r r r r r r r r r r r r r r r r																
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0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	517	516	516	515	514	514	513	513	513	512	511	510.5	510	510	508.5	507.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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	RESULT 1	
	Ig heavy ch	Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fra
	C;Species:	C, Species: Homo gapiens (man)
	C;Date: 19-Dec-1993 C:Accession: A49047	Cibate: 19-Dec-11993 #Bequence_revision 18-Nov-1994 #text_change 20-Mar-1998 Cibatession: A49044
_	R, Victor, K	Rivictor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
	Eur. J. Immi	unol. 22, 2231-2236, 1992
	A; Title: Hur	A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes o
_	A; Reference	A; Reference number: A49047; MUID: 92387224; PMID: 1516616
_	A; Accession: A49047	: A49047
	A;Status: preliminary	reliminary
	A;Molecule t	A; Molecule type: nucleic acid
	A;Residues:	A;Residues: 1-136 <vic></vic>
_	A; Cross-ref	A;Cross-references: UNIPARC:UP10000176C6A
	A; Experiment	A; Experimental source: thymic B lymphocytes
	A;Note: seq	A;Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBIP:113207)
	C;Superfami.	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	F;19-102/Dot	F;19-102/Domain: immunoglobulin homology <imm></imm>
	Query Match	87.2%;
	Best Local	Best Local Similarity 87.4%; Pred. No. 6.9e-48; Matches 118: Conservative 4: Mismatches 4: Indels 9: Gans 3:
_		יידפוויים כולים ביי דוויכרים יי
	ò	1 EVOLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
	qa	5 BVQLVQSGABVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 64
		The control of the co
	Š	ol Syskyddydlisdaldsisiath. Chwsbirth. Ashar y Carlor Carl
	Dp qq	65 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQSYGYXDFRSGYYPAYYYY 121
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121 QGTTVTVSS 129
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115 RGTLVTVSS 123
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S38492
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: C36006
                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                           SPSFOGOATISADKSISTAYLOWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARSISSSG----YYSNFDYWG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (clone DOB) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
;Accession: C36006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSFQCQATISADKSISTAYLQWSSLKASDTAMYYCARH----VDVGATIGGYYYYYHGMD
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                                                                                                                                                                                                                                          1 EVOLVOSGAEVKKPGESLKISCKGSGYSFITYWIAWVROMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                       EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: PH1558
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Accession: PH1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                       Length 134;
                    A,Note: the authors translated the codon ATG for residue 93 as C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000176B81
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                               Indels
                                                                                                                     84.0%; Score 587.5; DB 2;
85.6%; Pred. No. 6.4e-46;
iive 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI0000176C49; GB:M34022
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C36006
IG heavy chain V region (83p2) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision
C;Accession: C36006
                                                                                                                                      Best Local Similarity 85.6
Matches 113, Conservative
                                                                                                                                                                                                                                                                                                                                                                    VWGQGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                         VWGKGTTVTVSS 130
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Matches 110; Conservative
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source: PBMC
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A; Residues: 1-123 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-139 < RAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
  A; Experimental
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A;Reference number: PH1428
A;Accession: PH1428
A;Accession: PH1428
A;Accession: PH1438
A;Residues: 1-113 <VAN>
A;Residues: 1-113 <VAN>
A;Residues: 1-113 <VAN>
A;Cross-references: UNIPARC:UPI0000176B77; GB:S51905; NID:9262690; PIDN:AAC80261.1; PID:90.2;Reywords: heterotetramer; immunoglobulin immunoglobulin phomology
E;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38492 #sequence_revision 06-Jan-1993
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a ph A;Reference number: S38488
A;Reference number: S38492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARH---NSQTGASLWYF---DLWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AFDVWG 104
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                        Length 123
A,Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterzemer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                  Score 574; DB 2;
Pred. No. 9.6e-45;
                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                            82.1$;
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Matches 109; Conservative
                                                                                                                                                                                                                        Query Match 82.1
Best Local Similarity 85.3
Matches 110; Conservative
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A,Cross-references: UNIPARC:UP10000116462; EMBL:Z14183; NID:g31033; PIDN:CAA78552.1; PID. CS,Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin homology <!-- The content of the 
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SPSFQGQVTISADESISTAYLQWSSLKATDTAMYYCARR-DYGD-----YQSTGGFDPWG 114
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S31685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHIS61

Ig heavy chain V region (clone CAV) - human (fragment)

C;pecies: Homo sapiens (man)

C;pecies: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000

C;Accession: PHIS61

R;Rassenti, L.Z.; Kipps, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A;Title: Lack of extensive mutations in the VHS genes used in common B cell

A;Reference number: PHIS57; MUID:93210459; PMID:7681468
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   A;Cross-references: UNIPARC:UPI000017694E
A;Experimental source: PBMC
A;Note: the authors translated the codon TTG for residue 119 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 141;
                                                                                                                                                                                                                                                     Length 127;
                                                                                                                                                                                                                                                                                                                     11; Indels
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                                                                                                                                                                                                                                              Query Match
79.8%; Score 558; DB 2;
Best Local Similarity 84.5%; Pred. No. 2.7e-43;
Matches 109; Conservative 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 553.5; DB 2
Pred. No. 7.7e-43;
3; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.9%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGTTVTVSS 129
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KGTTVTVSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-141 <CUI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: PH1561
A,Molecule type: DNA
A,Residues: 1-147 <RAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PH1563
R;Rassenti, L.Z.; Kipps, T.J.
J; Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymp
A;Reference number: PH1557; MUID:93210459; PMID:7681468
                                                                       A;Cross-references: UNIPARC:UP1000011654D; EMBL:Z23034; NID:g414031; PIDN:CAA80569.1; PI CS.Superfamily: immunoglobulin V region; immunoglobulin homology. C;Reywords: heterotetramer; immunoglobulin C;Reywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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R; van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHG--MDV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARR-----RYSYAQHDWYFDL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPSFQGHVTISADKSISTAYLQWSSLKASDTAMYYCARLLYGAAAAWGYYYYY--MDVWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (clone P1-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                 Score 561; DB 2; Length 12
Pred. No. 1.4e-43;
3; Mismatches 9; Indels
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A;Reference number: PH1409; MUID:93115676; PMID:8418213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (clone PET) - human (fragment)
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                                                                                                                                                                                                                                                     80.3%;
83.2%;
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KGTTVTVSS 144
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A; Molecule type: DNA A:Pesidues: 1-123 < MAR>
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A; Residues: 1-127 <VAN>
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A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                     109;
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Best Local S
Matches 109
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A; Cross-references: UNIPARC: UPI000017694F
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Best Local Similarity 82.2%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QGTTVTVSS 129
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A; Residues: 1-136 <RAS>
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A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
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                                                                                                                                                                  Query Match
                                                                                                                                                                                          Best Loca
Matches
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PH1415
Ig heavy chain V region (clone P1-57) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
R;Accession: PH1415
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone P3-9) - human (fragment)
C;Species: Homo saplens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1423
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of
                                                                                                                                                                                                                                                                                                                                78 SPSFQGHVTISADKSISTAYLQWSSLKASDTAMYYCARQIAGIAAAGMWGPYYYYY-MDV 136
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                                                                                                                                                                                                           EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels 10; Gaps
                                                                                                                                                                3;
                                                                                                                       Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.3%; Score 547; DB 2; Length 123; Best Local Similarity 80.6%; Pred. No. 2.6e-42; Matches 104; Conservative 4; Mismatches 11; Indels
                          Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAIYYCARHAD-
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A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1423
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A;Accession: PH1415
A;Mcocsolie type: mRNA
A;Residues: 1-127 <VAN>
                                                                                                                  Query Match 79.0%; Score 552.5; DB 2; Best Local Similarity 83.2%; Pred. No. 9.9e-43; Matches 109; Conservative 4; Mismatches 15;
                            C;Superfamily: immunoglobulin V region; immunog
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
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A,Residues: 1-123 <VAN-
A,Cross-references: UNIPARC:UP10000176B98
A,Experimental source: PBMC
  A; Cross-references: UNIPARC: UPI0000176961
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C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PHISS;
R;Rassenti, L.Z.; Kipps, T.J.
R;Rassenti, L.Z.; Kipps, T.J.
A;Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph A;Reference number: PHISS7; MUID:93210459; PMID:7681468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: PH1420
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
T. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 EVQLVQSGAEVKKPGESLKISCKGSRYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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9
A.Experimental Source: PBMC
A;Note: the authors translated the codon TTG for residue 118 as lo. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                         Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 136;
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Keywords: heterotetramer; immunoglobulin
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A;Reference number: PH1409; MUID:93115676; PMID:8418213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (clone HAN) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 2;
Pred. No. 3.5e-42;
2; Mismatches 11
                                                                                                                                                                                                                     / Match 78.1%; Score 546; DB 2; Local Similarity 83.7%; Pred. No. 3.3e-42; nes 108; Conservative 2; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPARC:UPI0000176A21
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RESULT 15
PH419
Ig heavy chain V region (clone P2-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH419
R;van der Stocp, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SPSFQGQVTISADKSISTAYLQWSSLRASDTAIYYCARHGLHGTSFSSWF-----DFWG 114
                                                                                                                                                                                                                                                                                                                                                                                                    SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                A,Noče: the authors translated the codon CTT for residue 101 as Phe C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Note: the authors translated the codon ACT for residue 107 as Ser C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                Query Match 78.0%; Score 545; DB 2; Length 127; Best Local Similarity 79.8%; Pred. No. 4e-42; Matches 103; Conservative 8; Mismatches 12; Indels
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Best Local Similarity 79.1%; Pred. No. 6.7e-42;
Matches 102; Conservative 9; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 25, 2007, 04:06:39 Job time: 9.83898 secs
A;Cross-references: UNIPARC:UPI0000176B9A
A;Experimental source: PBMC
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A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UP10000176953
A;Experimental source: PBMC
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115 RGTLVTVPS 123
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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 03:58:23 ; Search time 88 Seconds (without alignments) 1574.822 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-665-383-38 699 1 BVQLVQSGAEVKKPGESLKI.......XYXYHGMDVWGQGTTVTVSS 129

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

3281787 segs, 1072124677 residues Searched:

3281787 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot\_sprot:\*
2: uniprot\_trembl:\* UniProt\_8.4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKIES	
Result		Query				
No.	Score	Match	Match Length	BB	qı	ion
н	4	3.2		7	Q5RE17 PONPY	EAG obuod
7	435.5	62.3	159	~	Q96QS0_HUMAN	Q96qs0 homo sapien
Э	418.5	59.9	118	~	Q9Z1C4 MOUSE	-
4	407	58.2	479	~	Q3KQK2_MOUSE	Q3kqk2 mus musculu
ហ	403	57.7	244	7	Q652C8_HUMAN	Q65zc8 homo sapien
9	398	56.9	483	~	Q52L51_MOUSE	SUM
7	395	56.5	614	~	Q7TMT6_MOUSE	Q7tmt6 mus musculu
80	394	56.4	458	~	Q5BJZ2_RAT	Q5bjz2 rattus norv
თ	392.5	56.2	617	7	Q4KML5 MOUSE	O4kml5 mus musculu
10	391.5	56.0	124	7	Q9UL92 HUMAN	Q9u192 homo sapien
11	391.5	56.0	613	~	Q8VCX7 MOUSE	_
12	390.5	55.9	200	7	Q9BRV0 HUMAN	Q9brv0 homo sapien
13	389.5	55.7	143	~	Q924P9_MOUSE	mus m
14	388	55.5	468	N	OS69W9 MOUSE	Q569w9 mus musculu
15	387	55.4	121	Н	HV01 MOUSE	P01745 mus musculu
16	386.5	55.3	143	~	Q91V67 MOUSE	Q91v67 mus musculu
17	385.5	55.2	498	~	Q6N041 HUMAN	Q6n041 homo sapien
18	384.5	55.0	145	~	Q924Q6_MOUSE	_
19	384	54.9	119	~	Q9UL94_HUMAN	Q9ul94 homo sapien
20	383	54.8	168	7	Q8VDC9_MOUSE	Q8vdc9 mus musculu
21	382.5	54.7	143	7	Q924Q5_MOUSE	Q924q5 mus musculu
22	382.5	54.7	482	~	Q2T9K9_MOUSE	Q2t9k9 mus musculu
23	382.5	54.7	590	~		Q4v9v8 mus musculu
24	382	54.6	125	7	Q9UL95_HUMAN	Q9ul95 homo sapien
25	382	54.6	146	~	Q924Q3_MOUSE	mus m
56	382	54.6	474	N	Q8R3H6 MOUSE	Q8r3h6 mus musculu
27	382	54.6	481	7	Q91WT1 MOUSE	Q91wt1 mus musculu
28	381.5	54.6	145	7	Q924R4_MOUSE	Q924r4 mus musculu
29	381	54.5	142	~	Q924Q2_MOUSE	Q924q2 mus musculu
30	381	54.5	144	~	Q924P5 MOUSE	Q924p5 mus musculu
31	381	54.5	470	7	Q7TMK1_MOUSE	Q7tmk1 mus musculu

Q924r3 mus musculu Q3syj4 mus musculu Q924r8 mus musculu Q924q0 mus musculu Q924q0 mus musculu Q94r32 mus musculu Q924r1 mus musculu Q925s3 mus musculu Q925r1 homo sapien Q569jf homo sapien Q569y0 rattus norv P01751 mus musculu Q924r7 mus musculu Q924r7 mus musculu Q924r7 mus musculu
0924R3 MOUSE 03SY14 MOUSE 0924R8 MOUSE 092400 MOUSE 092409 MOUSE 092409 MOUSE 092402 MOUSE 0924R1 MOUSE 09253 MOUSE 09253 MOUSE 09253 MOUSE 09253 MOUSE 0924R1 MOUSE 0924RT MOUSE 0924RT MOUSE 0924RT MOUSE
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					į	Schupp I., Wellenreuther er A., Fobo G., Han M., Wie	nk/DDBJ databases. the beta-chain of major	ly simi	ooo bttm://www.unintot	NoDer:	1			5	antigen:	processing, endogenous antigen											. 44		neng cu	Indels
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PRELIMINARY; PRT; 475 AA. integrated into UniProtKB/TrEMBL sequence version 1.		Verte				Poustka A., Albert R., Moosmayer P., Schupp I., Mewes H.W., Weil B., Amid C., Osanger A., Fobo	k/DDBJ he bet	molecu	1 4	ace mu Attrib	1 1 1 1 1		IEA.	IEA.	endog	ndogen										domain; Membrane;	0488780963277529	2	4	sec
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PRT; UniPro	C2335.	ngutan). Chordata, Craniata, Enarchontoglines. P				yer P. Osanç	itted (NOV-2004) to the EMBL/GenBa FINCTION: Beta-2-microglobulin is	x clas	# 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Distributed by the Unified Consolvium,		CR857722; CAH89990.1; -; mKNA. SER17: 21-475	C:integral to membrane; IEA.	IEA.	F:MHC Class I receptor a P:antiden presentation:	cessir		<u>:</u>			- smo-				NOMON	Hypothetical protein; Immunoglobulin	14.00	7 177	Pred. No.	
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PRELIMINARY, PR integrated into Uni sequence version 1.	entry version 19. protein DKFZp469C2335 C2335;	Metazoa;	minid 0;	SEQUENCE.	A Con	bert il B.	-2004 Beta-	tibil	the Haid	der t		; CAH					IPR007110;	IPR003006:	IPR003599;	IPR013106;	12KUU3596; 1 654; Cl-set;	>	; 16; 1. : 16c1:	ä	35; I(	rotei	ne. 475 AA.	Ĭ	rity	Conservative
	6	maeus 1; Met Euth	ii; Ho D=960	B SEC	n cDN	.; Al	VON) 1	сошра	707	ed to	1 0	OSEE17: 21	GO:0016021;	GO:0016020;	GO: 0030106;	1 ~1					7	PF07686;	SM00409;	SM00406;	PS50835;	cal p	rane.		Similarity	
T 1 7 PONPY QSRE17 PONPY QSRE17; 21-DEC-2004, 21-DEC-2004,	27-JUN-2006, entry Hypothetical protei Name=DKFZp469C2335;	Pongo pygmaeus (Orangutan). Eukaryota, Metazoa, Chordat Mammalia, Rutheria, Ruarcho	Catarrhin; Hominidae; CEL TaxID=9600;	LIJ NUCLEOTIDE TIGHT WAS AL	Tissus=Kidney; The German cDNA Consortium;	stka p es H.W	nitted		Construction has the Haiden	ribut		_	90:05			GO: 0019885;	InterPro;	InterPro; InterPro;	InterPro;	InterPro;		Д		S S	PROSITE;	theti	Transmembrane	1	arcii scal S	w
ULT 1 E17 PONP Q5RE17 Q5RE17 21-DEC	27-1 Hypk Name	Pone Euke	Cat	NUCL	The	Pour	Sup.			Diat		EMBL;	8	8	3 8	8	Inte	Inte	Inte	Inte	Pfam;	Pfam;	SMART;	SMART;	PROS	Hyp	Trai		Guery March Best Local	Matches
RESULT QSRE17 ID Q AC Q DT 2 DT 2	g g g	800	888	2	หือ	<b>8</b> 8	¥ 5	ខ្ល	ပ္ပင်	ខ្ល	ខ្លួ	3 5	ă	я В	ž	ä	a E	ž 5	ă	품 :	žä	88	ž č	i E	Д Б	ž	<b>₹</b> 6	3 3	žἄ	ž

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Mol. Immunol. 34:441-452(1997).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
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musculus (Mouse).
                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                           endothelial cells.",
                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                              STRAIN=Balb/c
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SEOUENCE
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                                                                                                                                                           120
                                                                                                                                                                                                SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDV---GATIGGYYYYYHGMD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 SQKFQGRLTWIRDISISIVYMDLSSLRSDDIAVYFCAREMEITFGGAVSKGFYYY--GMD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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Distributed under the Creative Commons Attribution-NoDerive License
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                                                                20 DIQLVQSGAEVKRPGESLRISCKGSGYTFTDYWIGWVRQMPGKGLELMGMIDPSNSGTKY
                                                                                                                                                              61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG
                                 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogic4 MOUSE PRELIMINARY; PRT; 118 AA.
0921C4.
01-MAY-1999, integrated into UniProtKB/TrEMBL.
01-MAY-1999, sequence version 1.
18-ARR-2006, entry version 22.
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01869; JAEC.

InterPro; IPR007110; Ig-like.

InterPro; IPR0031306; Ig-sub.

InterPro; IPR003596; Ig_wbet.

InterPro; IPR003596; Ig_wbet.

InterPro; IPR003596; Ig_wbet.

InterPro; IPR00406; Ig, 1.

INTERPRO; INTERPRO; IGW; I.

INTERPRO; 
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
78-RR-2006, entry version 21.
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY039025; AAK82649.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96QSO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 VWGQGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 VWGQGTTVTVSS 149
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                                                                                                                                                                                                                                                                                              121 QGTTVTVS 128
                                                                                                                                                                                                                                                                                                                                                              137 QGTLVIVS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Q921C4 MOI
ID Q921C
AC Q921C
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DT 18-AC
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996 OSO I
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQVQQSGABLARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                                                                                               Mueller J.F., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P. Matis L.A., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Gaps
                                                                                                                                                                                                                                                                        MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 59.9%; Score 418.5; DB 2; Local Similarity 58.9%; Pred. No. 6.6e-35; hes 76; Conservative 23; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q3KQK2 MOUSE PRELIMINARY; PRT; 479 AA. Q3KQK2; (100 Mouse) integrated into UniProtKB/TrEMBL. 08-NOV-2005, sequence version 1. 27-JUN-2006, entry version 8. Hypochetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U78801; AAD00293.1; -; mRNA.
HSSP; P01751; 1NQB.
SMR; Q921C4; 1-118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001110; Ig-like.
InterPro; IPR001559; Ig sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR03596; Ig_V-set.
Pfam; Pf07686; V-set; 1.
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EMBL, V13057; CAA73500.1; -; mRNA. InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig-sub. InterPro; IPR013106; Ig-V-set. InterPro; IPR033596; Ig-V-set_sub. Pfam; PF07686; V-set; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2005, sequence version 1.
27-JUN-2006, entry version 16.
LOC544903 protein.
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          18-APR-2006, entry version 10.
Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                  Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.9°
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QGTTVTVSS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain
                                                                        Homo sapiens (Human).
                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=LOC544903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q52151_MOUSE
Q52151;
                                                       Name=scFv;
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NON TER
SEQUENCE
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019883; P:MHC class I receptor activity; IEA.

R GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

R GO; GO:0019883; P:antigen processing, endogenous antigen via . .; IEA.

R GO; GO:0019883; P:antigen processing, endogenous antigen via . .; IEA.

R InterPro; IPR00110; Ig-1:et.

R InterPro; IPR001309; Ig-ub.

R InterPro; IPR013106; Ig-wet.

R InterPro; IPR013106; Ig-wet.

R InterPro; IPR013106; Ig-wet.

R Ffam; PR07666; V-set; 1.

R SMART; SM00409; IG; 2.

R R SMART; SM00406; IGV; 1.

R PROSITE; PS00835; IG_LIKE; 4.

R PROSITE; PS00835; IG_LIKE; 4.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunzante P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W. Sodergren E.J., Lu X., Gibbs R.A.,

Raby J., Helton E., Ketteman M., Madan A., Robrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:
----TFYF---DSWG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Immunoglobulin C region; Immunoglobulin domain; SEQUENCE 479 AB: 51746 Mar. necessary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLQQSGAELASPGASVKFSCKASGYTFTSYWMQWVKQRPGQGLEWIGAIYPGDGETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 407; DB 2; Length 479; 58.9%; Pred. No. 5.1e-33; ive 20; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 SQKVKGKATLTADKSSSTAYMQLSSLASEDSAVYCAR-----
                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2004, integrated into UniProtKB/TrEMBL, 11-OCT-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 58.98 es 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 OGTTLTVSS 134
                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0652CB HUMAN
0652CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
Q652C8 HUMAN
ID Q652C8 H
AC Q652C8;
DT 11-OCT-20
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Matches

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-Noberivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN-Mix FVB/N; TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.
Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 403; DB 2; Length 244; 58.9%; Pred. No. 6e-33; Live 23; Mismatches 22; Indels
                                                                                                                                                                                                                     MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629; Kontermann R.E., Wing M.G., Winter G.; "Complement recruitment using bispecific diabodies."; Namer. Biotechnol. 15:629-631(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2005, integrated into UniProtKB/TrEMBL
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Name=Igh-6; Synonyms=MGC60843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMBL; BC094065; AAH94065.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:001016020; C:membrane; IEA.
GO; GO:00101086; F:MHC class I receptor activity; IEA.
GO; GO:0010883; P:antigen presentation, endogenous antigen; IEA.
GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig Cl-set.
InterPro; IPR003599; Ig GMHC.
InterPro; IPR0013599; Ig Sub.
InterPro; IPR013106; Ig V-set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 OLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ÓLÓGSGAERVKPGASVKISCKASGYAPSGPWMNWVKÖRPGKGLEWIGRIYPGDGETHYSG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schwitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 56.9%; Score 398; DB 2; Length 483; Local Similarity 59.1%; Pred. No. 4.4e-32; and 75; Conservative 20; Mismatches 22; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG HIC; UNKNOWN 2.
PROSITE; PS00290; IG MIC; UNKNOWN 2.
Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 AA; 52167 MW; COFDB9168795FEB4 CRC64;
                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF07654; C1-set; 2. Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q7TMT6 MOI
1D Q7TM
AC Q7TM
DT 01-00
DT 25-JI
DE MGC6
        요
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01-OCT-2003, integrated into UniProtKB/TrEMBL. 01-OCT-2003, sequence version 1. 02-ULL-2006, entry version 31. MGC60843 protein.

614 AA.

Q7TMT6 MOUSE PRELIMINARY; PRT; Q7TMT6;

MOUSE

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MISSP: PO1820; 1074.

MGI; MGI:96448; 1gh-6.

MGI; MGI:96447; 1gh-6.

MGI; MGI:9647; 1gh-6.

MGI; MGI:9647; 1gh-6.

MGI; MGI:9648; 1gh-6.

MGI; MGI:964; 1gh-6.

MGI:964; 
                                                                                                                                                                                                                                                                                                                                                EXPAIN=CS7BL/GNCT: TISSUB=Hematopoietic Stem Cell;

RX PubMed=12477932, DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

RA Hopkins R.F., Gaares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schwochenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schwulus D.E., Schnerch A., Schein J.B.,

RA Glibs R.M., Maria M.A.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

RA Rodriguez C.M. Balska J. B. B.,

RA Rodriguez C.M. Ballska J. B.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez C.M. Ballska J. B.,

RA Rodriguez C.M. Ballska J. B.,

RA Rodriguez C.M. Ballska J. B.,

RA Rodriguez C.M. Ballska J. 
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                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6NCr; TISSUE-Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC053409; AAH53409.1; -; mRNA.
                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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WWW WIND DRAW BRANKER BRANK BR
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Q4KML5_MOUSE
ID Q4KML5_MOUSE
AC Q4KML5;
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Matches
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Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Altschul S.P., Jordan H., Moore T., Max S. I., Wang J., Heishe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broaks S.A., McKernan F.J., McKernan R.J., Malk J.A., Gunzartne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
M. Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
M. Schein J.E., Jones S.J.M., Marra M.A.;
M. Manne C.M., Schein J.E., Jones S.J.M., Marra M.A.;
M. Manne C.M., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                   1 EVQLVQSGAEVKKPGESLKISCKGSGYSPTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                  Gaps
                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Thymus;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                              56.5%; Score 395; DB 2; Length 614; 58.1%; Pred. No. 1.2e-31; ive 23; Mismatches 21; Indels
839BAF3B8D124F89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                              05BJZ2;
12-APR-2005, integrated into UniProtKB/TrEMBL.
12-APR-2005, sequence version 1.
27-JUN-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                    458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC091272; AAH91272.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY; PRT;
67747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein (By similarity).
               Query Match
Best Local Similarity 58.13
The 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                 QGTTVTVSS 129
                                                                                                                                                                                                                                                                  OCTLVTVSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q5BJZ2; 21-454
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOC367586 protein.
Name=LOC367586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissue=Thymus;
                                                                                                                                                                                                                                                                                                                                                  QSBJZ2_RAT
                                                                                                                                                                                                 80
SEQUENCE
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strandberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Strandberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Alausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusnia K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guinarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Wurny D.M., Sodergren B.J., Lu X., Gibbs R.A., Pahesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQSGABLVKPGSSVKISCKASGYTFTNYDIHWIKQQPGNGLEWIGWIYPGNGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                              56.4%; Score 394; DB 2; Length 458; 56.6%; Pred. No. 1.1e-31; ive 21; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2005, integrated into UniProtKB/TrEMBL. 02-AUG-2005, sequence version 1. 27-JUN-2006, entry version 11.
InterPro; IPR003597; Ig_C1-set.
InterPro; IPR003599; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set_sub.
Pfam; PP07654; C1-set; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus
                                                                                                                                           SMART; SM00409; IG; 1.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       Local Similarity 56.6%
nes 73; Conservative
                                                                                            Pfam; PF07654; Cl-set; 3. Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 QGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGVMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                     EMBL; AF035022; AAD56258.1; -; mRNA.
                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR013599; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set_sub.
IRMRT; SMO0409; IG; 1.
IRMRT; SMO0409; IG; 1.
IRMRT; SMO0406; IGV; 1.
IRMRT; SMO0406; IGV; 1.
IRMRT; SMO0406; IGV; 1.
IRMUNOGlobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBVCX7_MOUSE PRELIMINARY; PRT;
Q8VCX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 58.0%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 WGOGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 WGOGTLVTVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                            P01751; 1NQB
                                                                                                                                                                          LinkHub; 09UL92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Igh-6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q8VCX7 MOU
ID Q8VCX
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                                                                         RMI, MGI:96448, 19h-6.

RGO:001081915; C:B cell receptor complex; IDA.

RGO:001081915; C:B cell receptor complex; IDA.

RGO:001081915; C:B cell receptor complex; IDA.

RGO:001081915; C:B centernal side of plasma membrane; IDA.

RGO:00108271; C:immunoglobulin complex, circulating; IDA.

RGO:0010823; F:antigen binding; IDA.

RGO:0010815; F:protein binding; IPA.

RGO:00108189; F:transmembrane receptor activity; IDA.

RGO:00108189; F:transmembrane receptor activity; IDA.

RGO:0010819; P:antigen processing; IDA.

RGO:0010819; P:antigen processing; IDA.

RGO:0010819; P:antigen processing; IDA.

RGO:0010819; P:antigen processing; IDA.

RGO:0010819; P:positive regulation of B cell proliferation; IDA.

RGO:00108199; P:positive regulation of endocytosis; IDA.

RGO:00108199; P:positive regulation of endocytosis; IDA.

RGO:001081991; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000, sequence version 1.
18-APR-2006, entry version 22.
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLQQSGAELAKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGYVNPSSGYTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50813; IGWILKE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN 3.
Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.2%; Score 392.5; DB 2; Length 617; 55.8%; Pred. No. 2.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR00110; IS-11ke.
InterPro; IPR00110; IG-11ke.
InterPro; IPR001059; IG-CI-set.
InterPro; IPR00106; IG-Mr.
InterPro; IPR001066; IG-W-set.
InterPro; IPR0013106; IG-V-set.
Fam: PF07654; CI-set; 4.
Pfam: PF07656; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL92_HUMAN PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.8 es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGTTVTVSS 129
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCAR--HVDVGATIGGYYYYYHGMDV 118
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X STRAIN-EVBAN; TISSUE-Salivary gland;

X MEDINE-2188257; PubMed-12477932; DOI-10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W. Worley N.M., Fodersten E.J., Lu X., Glabs R.A.,

X Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWYRQAPGQGLEWMGIINPSGGSTSY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
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124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%; Score 391.5; DB 2;
58.0%; Pred. No. 4.2e-32;
tive 19; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002, integrated into UniprotKB/TrEMBL. 01-WAR-2002, sequence version 1. 27-JUN-2006, entry version 33.
Clin. Immunol. Immunopathol. 87:184-192(1998)
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                   MUCLEOTIDE SEQUENCE.
MEDLINE=89110066; PubMed=2464031;
Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
Morrison S.L., Kabat E.A.;
"Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1---6) dextrans.";
J. Immunol. 142:888-893(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00409; IG; 1.
SWART; SM00400; IG; 1.
SWART; SM00400; IGv; 1.
SPROSTIE; PS50815; IG LIKE; 5.
PROSITE; PS00290; IG WHC; UNKNOWN 3.
Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Mismatches 24; Indels
                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                    STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC018315; AAH18315.1; -; mRNA
                                                                            mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 57.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF07654; C1-set; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C30562; C30562.
                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01751; 1A6W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RC TISSUE=Prostate;

RX Pubmed=12477932; DDI=10.1073/pnas.242603899;

RA Mammalian Gene Collection Program Team,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Haish P.,

RA Altechul S.F., Zeeberg B., Boraldo M.F., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Stapleton M.J., Undin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Wckernan K.J., Malek J.A., Gunaratne P.H.,

RA Stapleton D.K., Muzny D.M., Sodergren B.J., Lu X., Glubaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rayminski M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Rand Maria M.A.;

Rand Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; IEA.
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                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensempl; ENGCO0000130076; Homo sapiens.

GO; GO:0016020; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0030106; F:MHC class I receptor activity; IEA.

GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

GO; GO:0019885; P:antigen processing, endogenous antigen via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                        01-JUN-2001, integrated into UniProtKB/TrEMBL. 01-JUN-2001, sequence version 1. 25-JUL-2006, entry version 36.
                            500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC005951; AAH05951.1; -; mRNA.
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InterPro; IPR013151; 19.
InterPro; IPR00351; 19-11ke.
InterPro; IPR003509; 19_MHC.
InterPro; IPR013509; 19_WHC.
InterPro; IPR013106; 19_V-set.
InterPro; IPR013106; 19_V-set.
Pfam; PP07654; 19_V-set_sub.
Pfam; PP07654; 19; 1.
Pfam; PP07684; 19; 1.
                         PRT;
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                         PRELIMINARY;
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                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                      GHA1 protein.
00 HUMAN
Q9BRVO_HUMAN
                                                                                                                                                                                  Name=IGHA1;
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73; Conservative 19; Mismatches
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Q569W9 MOUSE
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                                                                                                                                                                                                                                                            20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
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WEDLINE=95018259; PubMed=7523684;

WEDLINE=95018259; PubMed=7523684;

Pokkuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;

"Preparation, characterization and crystallization of an antibody Fab
fragment that recognizes RNA. Crystal structures of native Fab and
three Fab-mononucleotide complexes.";

J. Mol. Biol. 243:283-297(1994).
                                                                                                                                                                        Gaps
                                                                                                                                                                        3,
                                                                                                                 55.9%; Score 390.5; DB 2; Length 500; 56.9%; Pred. No. 2.7e-31; ive 21; Mismatches 32; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
PS50835; IG LIKE; 4.
PS00290; IG MHC; UNKNOWN 1.
500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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InterPro; IPR003599; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set.
Fam; PP07686; V-set; I.
SWART; SW00409; IG; I.
PROSITE; PS50835; IG_LIKE; I.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB069916; BAB63932.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q924P9 MOUSE PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V303-D-J-C mu protein (Fragment)
Name=V303-D-J-C mu;
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                                                                                                                                                                        74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GQGTTVTVSS 129
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138 GKGTTVTVSS 147
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PIR; PH1161; PH1161.
PIR; PH1162, PH1162.
PIR; S53751; SS3751.
HSSP; P01751; 1A6W.
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                                                                                                                                             Local Similarity
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                               PROSITE; 1
SEQUENCE
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     PROSITE;
                                                                                                                 Query Match
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DD O924P
AC O924P
DD O1-DB
DT O1-DB

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Score 389.5; DB 2; Length 143; Pred. No. 8e-32;

55.7%;

Best Local Similarity

Query Match

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Arose spontaneously,
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B.B., Wedner L., Marchine G.D.,
Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., McDuley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                    61 NQKFKGKATLITVDISSSTAYMQLSSLISBDSAVYYCASH-----YYGSSSDYWG 109
                                                                                                                           61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                       1 EVOLVOSGABVKKPGESLKISCKGSGYSFTSYWIGWVROMPGKGLEWMGIIYPGDSDTRY
11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Czech II; TISSUE-Mammary tumor metastatized to lung. Tumor
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STRAIN=C2ech II; TISSUE=Mammary tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMR; 0569W9; 20-464.

MGI; MGI:86443; Igh-la.

GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.

GO; GO:0005771; C:immunoglobulin body; IDA.

GO; GO:0001788; P:antigen binding; IDA.

GO; GO:0001788; P:antigen processing; IDA.

GO; GO:0001788; P:antigen processing; IDA.

GO; GO:000098; P:complement activation, classical pathway; IDA.
26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1. 27-JUN-2006, entry version 15.
                                                                                                                                                                                                                                                                                                                                                                   468 AA.
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                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
                                                                                                                                                                                                                                          110 OGTTLTVSS 118
                                                                                                                                                                                                                 121 OGTTVTVS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Igh-la protein.
                                                                                                                                                                                                                                                                                                                                                             Q569W9_MOUSE
Q569W9;
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Search completed: April 25, 2007, 04:06:35 Job time : 89.822 secs
                                                                                                                                                             InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.6%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QGTTVTVSS 129
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G0:0006911; P:phagocytosis, engulfment; IDA.
G0:0006910; P:phagocytosis, recognition; IDA.
G0:005078; P:positive regulation of B cell activation; IDA.
G0:0050778; P:positive regulation of immune response; IDA.
G0:0050776; P:positive regulation of phagocytosis; IDA.
G0:001812; P:positive regulation of type I hypersensitivity; IDA.
G0:001798; P:positive regulation of type IIa hypersensit. . .; IDA.
G0:0030162; P:regulation of proteolysis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EVQLQQSGAELVRPGSSVKLSCKTSGYTFTSYYINWVKQRPGQGLEWIGHIYPGNGYTEY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVOLVOSGABVKKPGESLKISCKGSGYSFTSYWIGWVROMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
--- MISCELLANEOUS: This sequence was translated from an mRNA isolated from a myeloma that secretes 1gG2b.
--- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                         R InterPro; IPR007110; Jg-11ke.
R InterPro; IPR003101; Jg-11ke.
R InterPro; IPR003505; Jg_C1-set.
R InterPro; IPR003505; Jg_C1-set.
R InterPro; IPR003505; Jg_WhC.
R InterPro; IPR003505; Jg_V-set.
R InterPro; IPR013106; Jg_V-set.
R Pfam; PF07654; C1-set; J.
R Pfam; PF07654; C1-set; J.
R SMART; SM00409; JG-1.
R SMART; SM00400; JG-1.
R SMART; SM00400; JG-1.
R PR0SITE; PS00230; JG_LIKE; 4.
R PR0SITE; PS00230; JG_MC; UNKNOWN 1.
R PROSITE; PS00230; JG_MC; UNKNOWN 1.
R PR0SITE; PS00230; JG_MC; UNKNOWN 1.
R PR0SITE; PS00230; JG_MC; UNKNOWN 1.
R PR0SITE; PS00230; JG_MC; UNKNOWN 1.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
  early endosome to late endosome transport; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.5%; Score 38%; DB 2; Length 46%; 56.6%; Pred. No. 4.5e-31; ive 24; Mismatches 22; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 AA; 51666 MW; 5BF6E527329F8461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 38. Ig heavy chain V region MPC 11. Mus musculus (Mouse).
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ERRATUM, AND SEQUENCE REVISION.
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Best Local Similarity 56...,
73; Conservative
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NUCLEOTIDE SEQUENCE.
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P01745;
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region MPC 11.
/FTId=PRO_000059868.
Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%; Score 387; DB 1; Length 121; 56.6%; Pred. No. 1.2e-31; ive 21; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
                                                                                                                                                                                            InterPro; IPR013106; Ig-V-set.
InterPro; IPR03596; Ig-V-set.
InterPro; IPR003596; Ig-V-set_sub.
Pfam; PP07686; V-set; 1.
SMART; SM00406; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region.
                                                                     HSSP; P01751; 1NQB.
SMR; P01745; 1-121.
Ensembl; ENSMUSG0000062635; Mus musculus.
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82.7%;
87.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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Sequence 133, App
Sequence 133, App
Sequence 32, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
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696.311 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/ EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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## ALIGNMENTS

UPEANLING SISLEM: FULLOS/NOS-LOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021 APPLICANT: Knappik, Achim
APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Ne Sequence 26, Application US/09025769B Patent No. 6300064 GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Score 578; DB 2; Length 119; Pred. No. 6.5e-48;

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61 SPSFQGQVTISADKSISTAYLQMSSLKASDTAMYYCAR---LGG--GGYYF-----DYWG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                 Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 578; DB 2;
Pred. No. 6.5e-48;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                            Sequence 26, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 26:
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Best Local Similarity 87.6%;
Matches 113; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ģĠŦĿŸŦŸSŚ 119
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                                                                       121 QGTTVTVSS 129
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                                                                                                                                         SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                            1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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                                                 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
    4; Indels 10; Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%; Score 578; DB 2; Length 119;
87.6%; Pred. No. 6.5e-48;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthur, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-490-070A-26
                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 26, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELEPHONE: (202) 912-2000
IELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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Matches 113; Conservative
    Matches 113; Conservative
                                                                                                                                                                                                                                                                              111 ÓGTLVTVSS 119
                                                                                                                                                                                                                                   121 OGTTVTVSS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                        US-09-490-070A-26
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                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.7%; Score 578; DB 2; Length 119; 87.6%; Pred. No. 6.5e-48; Live 2; Mismatches 4; Indels
           Sequence 26, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Raappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION UNBER: US/09/490,324
PILING DATE: CA-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
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INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10021
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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US-09-490-324-26
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Sequence 40, Application US/09025769B Patent No. 6300064

RESULT 5 US-09-025-769B-40

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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 10021 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
ANAK: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Go, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 571.5; DB 2;
Pred. No. 2.7e-47;
1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%;
86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212)596-900
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 86.8*
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-025-7698-40
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COMPUTER: IBM PC compatible
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US-09-490-070A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARW------GGDGFY--AMDYWG 111
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APPLICANT Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plucckthun, Andreas
TITLE OF INVENTIVE Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                     ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                   OPERATING SYSTEM: C-C-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 571.5; DB 2
Pred. No. 2.7e-47;
1; Mismatches 7
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: BP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY, AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-490-070A-40; Sequence 40, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.8%;
Matches 112; Conservative
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
  CORRESPONDENCE ADDRESS:
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                                                            CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                    STATE: Ne
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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STREET: 1666 K Street, N.W., Suite 300
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
RAPLICATION UNDER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 120;
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Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.8%; Score 571.5; DB 2; Best Local Similarity 86.8%; Pred. No. 2.7e-47; Matches 112; Conservative 1; Mismatches 7;
                                                                                                  FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
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COMPUTER READABLE FORM:
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FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/490,153
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                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
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Patent No. 6706484
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                           LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                            TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 67:
                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 571.5; DB 2; Length 1
Pred. No. 2.7e-47;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                   NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 67: US-09-490-070A-67
                                                                                                                                                          TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
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Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
86.8%;
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Best Local Similarity 86.8
Matches 112; Conservative
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ZIP: 10021
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                     1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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Length 120;
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                                                             Indels
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Pack, Peter
Ilag, Vic
Ge, Limino
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
Query Match 81.8%; Score 571.5; DB 2; Best Local Similarity 86.8%; Pred. No. 2.7e-47; Matches 112; Conservative 1; Mismatches 7;
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                                                                                                                                                                                                                                                                                                     61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARW------GGDGFY--AMDYWG 111
                                                                                                                                                                                                                               1 EVOLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
                                                                                                                                                                                          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: INP PC compatible
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION NUMBER: US/09/490,324
PILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave STREF: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                  Score 571.5; DB 2; Length 120;
Pred. No. 2.7e-47;
1; Mismatches 7; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40
                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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                                                                                                    Query Match
Best Local Similarity 86.8%;
Matches 112; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      112 OGTLVTVSS 120
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                                                           US-09-490-153-67
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Length 120;

DB 2;

81.8%; Score 571.5;

Query Match

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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                                                                                                                                                                                              61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARW------GGDGFY--AMDYWG 111
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                                                                                             1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                    EVOLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                        Gaps
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TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: THOUGH TO COMPATIBLE
COMPUTER: THOUGH TO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 18-REB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-REB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 120;
                      Indels
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86.8%; Pred. No. 2.7e-47;
tive 1; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Inaq, Vic
GG, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
Best Local Similarity 86.8
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                            121 QGTTVTVSS 129
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SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
                          61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARW-----GGDGFY--AMDYWG 111
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                                                                                                                                                                                                  RESULT 13
US-08-665-202-33
US-08-665-202-33
Sequence 33, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYW1GWVRQMPGKGLEWMG11YPGDSDTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BVOLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-70N-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-70N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 15-70N-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUMBER: TOWN 1995
ATTORNEY/AGENT INFORMATION:
NAME: HUMBER: TOWN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.0%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-33
                                                                                         QGTTVTVSS 129
                                                                                                                                    112 OGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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61
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61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR 98

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RESULT 14 US-09-315-574-33 ; Sequence 33, Application US/09315574

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
                                                                                                     No. 6512097el High Affinity Human Antibodies to
Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/665,202
FILING APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT IRPORMATION:
ANAMO: WINDER: TROWMATION:
ANAMO: WINDER: TOWNEY TOWNEY.
                                                                                                                       STREET: Majestic, Parsons, Siebert & Hsue P.C. STREET: Four Embarcadero Center, Sulte 1100 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.2%; Score 519; DB 2; Best Local Similarity 99.0%; Pred. No. 2.3e-42; Matches 97; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/10194975
Batent No. 6881557
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION VUMBER: 38,498
REFERRUCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Patent No. 6512097;
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512;
TITLE OF INVENTION: Tumor An, NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Flor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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0; Gaps
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                                                                                                                                                                                                                                                                                                                  Search completed: April 25, 2007, 04:08:30 Job time: 17.2161 secs
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-45
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APPLICANT: Jia, Xiao-Chi
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                                                                                                                                                                                                April 25, 2007, 04:18:18 ; Search time 48 Seconds (without alignments) 1251.741 Million cell updates/sec
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| BMC Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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| BMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| BMC Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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Sequence 13, Ap
Sequence 140, A
Sequence 29, Ap
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1 EVQLVQSGAEVKKPGESLKI......YYYYHGMDVWGQGTTVTVSS
                           GenCore version 6.2.1
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Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
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Best Local Similarity 100.0
Matches 129; Conservative
    121 OGTTVTVSS 129
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CORGANISM: homo sapiens
US-10-041-860-319
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; ORGANISM: homo sapiens
US-10-665-383-38
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                              APPLICANT: Gazii, tachard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2: PARTING APPLICATION NUMBER: 129
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100.0%; Pred. No. 2.4e-55;
trive 0; Mismatches 0;
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Yang, Xiao-Dong
Chen, Francine
ang, Xiao-Dong
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Weber, Richard
Bezabeh, Binyam
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Best Local Similarity 100.
Matches 129; Conservative
                          Chen, Francine
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SOFTWARE: FastSEQ for Win
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CORGANISM: homo sapiens
US-10-041-860-215
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CORGANISM: homo sapiens
US-10-041-860-250
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Best Local Similarity
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LENGTH: 129
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYY----YYHGM 116
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86.5%; Pred. No. 2.8e-46;
tive 1; Mismatches 6; Indels 11
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT PELLING DATE: 2012-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 313
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.9%; Score 593.5; DB 4; Best Local Similarity 85.7%; Pred. No. 7.8e-46; Matches 114; Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Best Local Similarity 86.5<sup>3</sup>
Matches 115; Conservative
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ORGANISM: homo sapiens
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APPLICANT: Treanor, James
APPLICANT: Treanor, James
APPLICANT: Huang, Haichun
APPLICANT: Huang, Haichun
APPLICANT: Inoue, Heather
APPLICANT: Zhang, Tie J.
APPLICANT: Zhang, Tie J.
APPLICANT: Martin, Frank
TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
TITLE OF INVENTION: Lihibitors
FILE REFERENCE: 02-1240
CURRENT PILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/487,431
PRIOR FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 125
                                                                                                                                                                                                                  SPSFQGQATISADKSISTAYLQMSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                        Length 129;
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88.4%; Pred. No. 1.1e-46;
.ive 7; Mismatches 4; Indels
                                                               0; Indels
                        Score 699; DB 4;
Pred. No. 2.4e-55;
                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       US-10-891-658-79; Sequence 79. Application US/10891658; Publication No. US20050074821A1; GENERAL INFORMATION:
                   Query Match
Best Local Similarity 100.0%;
Matches 129; Conservative 0
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
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Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Gazit, Gadi
Weber, Richard
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Matches 114; Conservative
                                                                                                                                                                                                                                                                               QGTTVTVSS 129
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US-10-041-860-313
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US-10-665-383-34
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Pred. No. 7.8e-46;
1; Mismatches 7; Indels 11;
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Pred. No. 7.8e-46;
1; Mismatches 7; Indels 11
y Sequence 214, Application US/10041860
y Bublication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Ocrvalan, Jose R.F.
APPLICANT: Grao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTIBODIES
TITLE OF LINGANTS ABGENTX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 214
LENGTH: 126
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Ghen, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
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Best Local Similarity 85.7%;
Matches 114; Conservative
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Best Local Similarity 85.7
Matches 114; Conservative
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; ORGANISM: homo sapiens
US-10-041-860-249
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61 SPSFQGQATISADKSISTAYLQMSSLKASDTAMYYCARHVDVGATIGGYYY----YYHGM 116
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                                                                   61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYY----YYHGM 116
                                                                                                  61 SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARH-----GSYYYGSETYYNVF 113
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                  1 EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
                                                                                                                                                                                                                                                     APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 593.5; DB 4;
Pred. No. 7.8e-46;
1; Mismatches 7;
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85.7%;
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                                                                                                                                          117 DVWGQGTTVTVSS 129
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Best Local Similarity 85.7
Matches 114; Conservative
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US-10-665-383-34
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                                                                                                                                                                                                              Query Match 84.8%; Score 592.5; DB 4; Length 126; Best Local Similarity 85.7%; Pred. No. 9.7e-46; Matches 114; Conservative 2; Mismatches 6; Indels 11;
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85.7%; Pred. No. 9.7e-46;
iive 2; Mismatches 6; Indels 11
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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX:051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: PASISEQ for Windows Version 4.0
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Matches 114; Conservative
                                                                                                               TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: homo sapiens
US-10-041-860-248
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                                                                        SEQ ID NO 23
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RESULT 14 US-10-041-860-300 Sequence 300, Application US/10041860 Publication No. US20030157109A1

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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYY----YYHGM 116
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85.7%; Pred. No. 9.7e-46;
ive. 2; Mismatches 6; Indels 11.
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Sequence 26, Application US/10665383
Publication No. US20040141969A1
GENERAL INFORMATION:
APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: Lichege, Juergen
APPLICANT: Lichentein, Henri
TITLE OF INVENTION: WEINO FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REFERENCE: AGGNIX.052A
CURRENT FILING DATE: 2003-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARR: FRASEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 126
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: WESTABH, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CORRENT
FILE REPRENCE: ASGRNIX. 051.A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
TENNETH. 100 300
TENNETH. 100 300
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Best Local Similarity 85.7%
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-300
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117 DVWGQGTTVTVSS 129 | ||||| ||||| 114 DYWGQGTLVTVSS 126

Search completed: April 25, 2007, 04:22:49 Job time : 48.7373 secs

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April 25, 2007, 04:23:02 ; Search time 50 Seconds (without alignments) 533.620 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodate//lpubpaa/US09_NEW_PUB.pep:*
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/EMC_Celerra_SIDS3/ptodate//pubpaa/US09_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/ptodate//lpubpaa/US10_NEW_PUB.pep:*
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1 EVQLVQSGAEVKKPGESLKI......YYYYHGMDVWGQGTTVTVSS 129
GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		109-181	109-1	109-1	11-109-181-31	JS-11-440-728-10	JS-11-440-728-14	US-11-440-728-22	US-11-440-728-14	440-7	440-7	440-7	1-440-728-90	US-11-109-181-31	440-7	440-7	11-440-728-6	440-7	.1-440-728-38	440-7	440-7	1-440-728-74	11-109-181-2	11-109-181	-11-109-181	-109-181
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æ	Query	100.0	100.0	100.0	100.0	87.8	87.8	87.0	87.0	86.8	86.1	86.1	85.7	85.6	85.6	85.6	85.5	85.4	85.3	85.2	85.1	85.0	84.9	84.9	84.9	84.8
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126 7 US-11-109-181-248 126 7 US-11-109-181-300 127 US-11-340-728-122 128 7 US-11-396-178-170 189 7 US-11-396-178-100 180 7 US-11-396-178-100 121 7 US-11-396-178-54 121 7 US-11-396-178-92 178 7 US-11-396-178-92 178 7 US-11-396-178-92 178 7 US-11-396-178-92 126 7 US-11-109-181-216 126 7 US-11-109-181-216 127 7 US-11-109-181-216 128 7 US-11-109-181-216 129 7 US-11-440-728-126 121 7 US-11-440-728-126 122 7 US-11-440-728-126 122 7 US-11-440-728-126 123 7 US-11-440-728-126 124 7 US-11-440-728-126 127 7 US-11-440-728-126	Sequence 248, App Sequence 300, App Sequence 122, App Sequence 176, App Sequence 177, App Sequence 157, App Sequence 94, Appl Sequence 92, Appl Sequence 216, App Sequence 216, App Sequence 102, App Sequence 126, App Sequence 126	Sequence 34, Appl
	US-11-109-181-248 US-11-109-181-300 US-11-396-178-170 US-11-396-178-175 US-11-396-178-175 US-11-396-178-175 US-11-396-178-157 US-11-396-178-157 US-11-440-728-94 US-11-396-178-92 US-11-396-178-92 US-11-396-178-153 US-11-109-181-251 US-11-109-181-251 US-11-109-181-251 US-11-109-181-251 US-11-109-181-37 US-11-440-728-102 US-11-440-728-126 US-11-440-728-126	11-440-728
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## ALIGNMENTS

TO PDGFD AND USES	DB 7; Length 129; 1.1e-57; les 0; Indels 0; Gaps 0;	EVOLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGMVRQMPGKGLEMMGIIYPGDSDTRY 60 	SPSFQGQATISADKSISTAYLQWSSLKASDTAMYVCARHVDVGATIGGYYYYYHGMDVWG 120 		
SULT 1  11-109-181-29  Sequence 29, Application US/11109181  Sequence 29, Application US/11109181  Sepulication No. US20060293506A1  GENERAL INFORMATION:  APPLICANT: Oravian, Jose R.F. APPLICANT: Feng, Xiao-Chi APPLICANT: Feng, Xiao-Chi APPLICANT: Gazit, Gadi APPLICANT: Gazit, Gadi APPLICANT: Gazit, Gadi APPLICANT: Bezabeh, Binyam TITLE OF INVENTION: ANTHRODIES DIRECTED T TITLE OF INVENTION: ANTHRODIES DIRECTED T TITLE OF INVENTION: THEREOF FILE REFERENCE: ABGENIX.051A CURRENT APPLICATION NUMBER: US/10/041,860  PRIOR FILING DATE: 2005-04-18  PRIOR FILING DATE: 2005-04-18  PRIOR FILING DATE: 2005-04-18  PRIOR PRILOR DATE: 2005-04-18  PRIOR PRIOR DATE: 2005-04	ch 100.0%; Score 699; cl Similarity 100.0%; Pred. No. 1. 129; Conservative 0; Mismatches	1 EVQLVQSGAEVKKPGESLKISCKGS 	61 SPSFOGOATISADKSISTAYLOWSS 	121 QGTTVTVSS 129           121 QGTTVTVSS 129	
RESULT 1 US-11-109-181-29 Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 20, Appl Sequ	Query Match Best Local Matches 12	oy Oy	oy Op	Oy 1	£

RESULT 2 US-11-109-181-215 ; Sequence 215, Application US/11109181

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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
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US-11-109-181-319
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION UNMER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
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                                                                                                              APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 699; DB 7;
Pred. No. 1.1e-57;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 699; DB 7; 100.0%; Pred. No. 1.1e-57;
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                                                                                                                                                                                                                                FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 250, Application US/11109181; Publication No. US20060293506A1; GENERAL INFORMATION:
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No. US20060293506A1
                              Corvalan, Jose R.F.
Jia, Xiao-Chi
                                                                             Feng, Xiao
Yang, Xiao-Dong
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Best Local Similarity 100.
Matches 129; Conservative
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ORGANISM: homo sapiens
US-11-109-181-250
                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: homo sapiens
US-11-109-181-215
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Best Local Similarity
                  GENERAL INFORMATION:
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LENGTH: 129
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LENGTH: 129
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                          1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: ADENIX.051A CURRENT APPLICATION NUMBER: US/11/109,181 CURRENT FILING DATE: 2005-04-18 PRIOR PILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE PARKERQ for Windows Version 4.0 SEQ ID NO 319 LENGTH: 129
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APPLICANT: GREEN, Larry L.
APPLICANT: YANG, Xiaodona
APPLICANT: YANG, Xiaodona
APPLICANT: QUEVA, Christophe
APPLICANT: BLAKEY, David Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABXAZ.003A
CURRENT APPLICATION NUMBER: US/11/440,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 319, Application US/11109181 Publication No. US20060293506A1 GENERAL INFORMATION:
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Publication No. US20070014720A1
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                                                                                                                                                                                                                                    87.8%; Score 614; DB 7; Length 121;
89.9%; Pred. No. 8.5e-50;
iive 2; Mismatches 3; Indels
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APPLICANT: GREEN, LAINTY L.
APPLICANT: VANG, Xiaodong
APPLICANT: QUENA, Christophe
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
FILE REFERENCE: ABXAZ.003A
CURRENT APPLICATION NUMBER: US/11/440,728
CURRENT FILING DATE: 2006-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
CURRENT FILING DATE: 2006-05-25
PRIOR APPLICATION NUMBER: US 60/686,992
PRIOR FILING DATE: 2005-06-02
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2005-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 143, Application US/11440728
Publication No. US20070014720A1
GENERAL INFORMATION:
APPLICANT: GAZIT-BORNSTEIN, Gadi
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Best Local Similarity 89.9'
Matches 116; Conservative
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                                                                                                    ; SEQ ID NO 10; LENGTH: 121; TYPE: PRT ; ORGANISM: Homo sapiens US-11-440-728-10
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Best Local Similarity
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LENGTH: 118
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US-11-440-728-22; Sequence 22, Application US/11440728

RESULT 7

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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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GENERAL INCOMENTATION:

APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: GREEN, Larry L.
APPLICANT: TANG, Xiaodong
APPLICANT: QUEVA, Christophe
APPLICANT: QUEVA, Christophe
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION NUMBER: US 60/686,992
PRIOR PILING DATE: 2006-06-02
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 121
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APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: TANG, Xiaodong
APPLICANT: QUEVA, Christophe
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABXAZ.003A
CURRENT APPLICATION NUMBER: US/11/440,728
CURRENT FILING DATE: 2006-02-5
PRIOR PILING DATE: 2006-06-05
PRIOR PILING DATE: 2005-06-02
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FASESEQ FOR Windows Version 4.0
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Pred. No. 3.1e-49;
1; Mismatches 2,
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Best Local Similarity 91.5%;
Matches 118; Conservative
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Matches 117; Conservative
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US-11-440-728-22
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US-11-440-728-145
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Query Match
Best Local Similarity 89.8%;
Matches 115; Conservative
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Best Local Similarity 89.13
Matches 115; Conservative
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ORGANISM: Homo sapiens
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  US-11-440-728-106
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US-11-440-728-90
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----NYYYGMDVWG 112
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Best Local Similarity 89.1%; Pred. No. 3.8e-49;
Matches 115; Conservative 2; Mismatches 4; Indels
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| Publication No. US20070014720A1 |
| GENERAL INFORMATION: US20070014720A1 |
| GENERAL INFORMATION: APPLICANT: GAZIT-BORNSTEIN, Gadi |
| APPLICANT: GREEN, Larry L. |
| APPLICANT: TANG, Xiaodong |
| APPLICANT: QUENCY, Christophe |
| APPLICANT: QUENCY, Christophe |
| TITLE OF INVENTION: THEREOF |
| PRIOR FILLING DATE: 2006-05-25 |
| PRIOR FILLING DATE: 2006-06-02 |
| PRIOR FILLING DATE: 2005-06-02 |
                                                                                                                                                                                                                        Sequence 18, Application US/11440728
Publication No. US20070014720A1
GENERAL INFORMATION:
APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: YANG, Xiaodong
APPLICANT: VANG, Xiaodong
APPLICANT: BLAKEY, David Charles
ITTLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
61 SPSFQGQVTISADKSISTAYLQWSSIKASDTAMYYCAR---VGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ABXAZ.003A
CURRENT APPLICATION NUMBER: US/11/440,728
CURRENT FILING DATE: 2006-05-25
PRIOR APPLICATION NUMBER: US 60/686,992
PRIOR FILING DATE: 2005-06-02
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 121
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US-11-440-728-106
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62 PSFQGQVIISADKSISTAYLQWSSLKASDTAMYYCAR------TGDYYSYHGMDVWGQ 113
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                                                                                                                                                                                                                                        62 PSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                          2 VOLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYS
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                                                                                                                  2 VOLVOSGAEVKKPGESLKISCKGSGYSFTSYWIGWVROMPGKGLEWMGIIYPGDSDTRYS
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                                                              8;
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Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencially Application US/11440728
; Sequencial No. US20070014720A1
; Publication No. US20070014720A1
; GENERAL INPORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: YANG, Xiaodong
; APPLICANT: PANG, Xiaodong
; APPLICANT: PROPENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ 003A
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR PLICHING DATE: 2006-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PRACESQ for Windows Version 4.0
; SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 90, Application US/11440728
Publication No. US20070014720A1
GENERAL INFORMATION:
APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: TANG, Xiaodong
APPLICANT: OUBVA, Christophe
APPLICANT: DIAKEN, David Charles
APPLICANT: TANG, XIAOTON: THEREOF
APPLICANT: TITLE OF INVENTION: THEREOF
Score 602; DB 7;
Pred. No. 1.1e-48;
0; Mismatches 5;
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FILE REFERENCE: ABXAZ.003A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SPSFQGQVIISADKSISTAYLQMSSLKASDTAMYYCARH------GSYYYGSETYYNVF 113
                                                                                                                                                                                                                                                                                                                                                                                              1 BVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60
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Pred. No. 2.5e-48;
1; Mismatches 6; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                         85.7%; Score 599; DB 7; Length 121; 88.4%; Pred. No. 2.1e-48; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Franchine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
CURRENT APPLICATION NUMBER: US/11/440,728
CURRENT FILING DATE: 2006-05-25
PRIOR APPLICATION NUMBER: US 60/686,992
PRIOR FILING DATE: 2005-06-02
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 313, Application US/11109181
Publication No. US20060293506A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 DVWGQGTTVTVSS 129
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                                                                                                                                                                                                                                                                                                                       Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 ÓGTTVTVSS 121
                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                Best Local Similarity
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Best Local Similarity
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US-11-109-181-313
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                                                                                                                                                                 LENGTH: 121
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61 SPSFQGQATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMDVWG 120
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              ; Sequence 146, Application US/11440728
; Publication No. US200700147201
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gad;
APPLICANT: GREEN, Larry L.
; APPLICANT: QAZIT-BORNSTEIN, GAD;
; APPLICANT: QAZIT-BORNSTEIN, GAD;
; APPLICANT: QUEAN, Christophe
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES;
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES;
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES;
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES;
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: ABXAZ.003
; CURRENT FILING DATE: 2006-05-25
; NUMBER OF SEQ ID NOS: 202
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FRELERE FEATER FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GAZITZON:
APPLICANT: GAZITZON:
APPLICANT: GAZITZON:
APPLICANT: GAZITZON:
APPLICANT: GAZITZON:
APPLICANT: VANG, Xiaodong
APPLICANT: VANG, Xiaodong
APPLICANT: WANG, Xiaodong
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ARAZ. 003A
CURRENT APPLICATION NUMBER: US/11/440,728
CURRENT APPLICATION NUMBER: US 60/686,992
PRIOR APPLICATION NUMBER: US 60/686,992
NUMBER OF SEQ ID NOS: 202
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
LENOTH: 1.21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.6%; Score 598; DB 7; Best Local Similarity 89.9%; Pred. No. 2.6e-48; Matches 116; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 598; DB 7;
Pred. No. 2.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/11440728
Publication No. US20070014720A1
GENERAL INFORMATION:
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ilarity 87.6%;
Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-146
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CORGANISM: Homo sapiens
US-11-440-728-98
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Best Local Similarity
Matches 113; Conserv
JS-11-440-728-146
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        Qy
        1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY 60

        Db
        1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWINWVRQMPGKGLEWMGIIYPGDSDTRY 60

        Cy
        61 SPSFQGQATISADKSISTAXLQWSSIKASDTAMYXCARHVDVGATIGGYXYXYHCMDVWG 120

        Cy
        61 SPSFQGQATISADKSISTAXLQWSSIKASDTAMYXCARHVDVGATIGGYXYXYHCMDVWG 120

        Db
        61 SPSFQGQVTISADKSINTAXLQWSSIKASDTAMYXCARQ------GGHYXYSGMDVWG 112

        Cy
        121 QCTTVTVSS 129

        Db
        113 QCTTVTVSS 121

        Search completed: April 25, 2007, 04:27:43

        Job time: 49.7415 secs
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protein search, using sw model . OM protein April 25, 2007, 03:54:56 ; Search time 98 Seconds Run on:

(without alignments)
564.248 Million cell updates/sec

US-10-665-383-40 590 Title: Perfect

1 DIVMTQSPLSLPVTPGEPAS.........MQALQSLMCSFGQGTKLEIK 113 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2782304 Potal number of hits satisfying chosen parameters:

2782304 segs, 489333398 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A\_Geneseq\_200701:\* 1: genesem'... geneseqp1990s:\* geneseqp2001s:\*geneseqp2002s:\* geneseqp2000s:\* Database

geneseqp2003as:\*geneseqp2003bs:\* geneseqp2005s:\* geneseqp2006s:\* geneseqp2007s:\* geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adk18831 Anti-huma	Adk18797 Anti-huma	-	Adl25430 Human mAb	Adk18898 Anti-huma	Aag65590 Anti-hEDR	Aay95221 Anti-plat	Aej57801 Human ant	Aej57944 Human ant	Aay95220 Anti-plat	Adi22126 Anti-plat	Aay95186 Anti-plat	Aay95226 Anti-plat	Adp47300 Human pho	Aek98277 Human 161	Aek98219 Human 161	Adi22125 Anti-plat	Adp03995 Murine-ex	Adi22111 Anti-plat	Adi22129 Anti-plat	Adi22112 Anti-plat	Aay95225 Anti-plat
ID	ADK18831	ADK18797	ADK18606	ADL25430	ADK18898	AAG65590	AAY95221	0 AEJ57801	0 AEJ57944	AAY95220	ADI22126	AAY95186	AAY95226	ADP47300	10 AEK98277	10 AEK98219	ADI22125	ADP03995	ADI22111	AD122129	AD122112	AAY95225
* Query Match Length DB	113 7	113 7	113 7	113 8	114 7	248 4	113 3	131 1	146 1	113 3	113 8	114 3	131 3	112 8		223 1	113 8	110 7	112 8	112 8	112 8	111 3
* Query Match 1	100.0	100.0	100.0	100.0	7.76	94.2	94.1	94.0	94.0	93.9	93.9	93.9	93.9	93.2	93.2	93.2	93.1	93.0	93.0	92.8	92.8	92.7
Score	590	590	290	590	576.5	256	555	554.5	554.5	554	554	554	554	550	550	550	549	548.5	548.5	547.5	547.5	547
Result No.	1	7	m	4	Ŋ	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22

Aay95187 Anti-plat	Adp47109 Human pho	Aea45169 Apolipopr	Aej64254 Human ant	Adi22114 Anti-plat	Aeh82673 Human ant	Aei93626 Human lig	Aej42800 IGF-R ant	Aej42864 IGF-R ant	Aej42818 IGF-R ant	Aek41374 Human imm	Aeh82663 Human ant	Aei65178 Anti-Ang-	Aeh82634 Human ant	Aeh82642 Human ant	Aeh82626 Human ant	Aeh82618 Human ant	Adv67311 Amino aci	Aei42744 Human imm	Aei62909 Human ant	Adp22370 Human ant	Adp46986 Murine li	Adj76892 Anti-IGF-
AAY95187	ADP47109	AEA45169	AEJ64254	ADI22114	AEH82673	AE193626	AEJ42800	AEJ42864	AEJ42818	AEK41374	AEH82663	AE165178	AEH82634	AEH82642	AEH82626	AEH82618	ADV67311	AE142744	AE162909	ADP22370	ADP46986	ADJ76892
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112	112	112	113	112	112	112	112	112	112	112	113	113	115	115	115	115	134	134	134	111	112	112
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8	92	92	92	92	92	92	92	92	8	92	92	92	92	92	92	92	92	92	92	92	92	92.
547	547	547	547	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546.5	546	546	545.5
23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

antiinflammatory; immunomodulator; cytostatic; gene therapy. Anti-human PDGF-D antibody protein related sequence #57. ADK18831 standard; protein; 113 AA (first entry) 06-MAY-2004 ADK18831; Ношо RESULT 1 ADK18831 

06-JAN-2003; 2003WO-US000398. 17-JUL-2003

WO2003057857-A2.

(ABGE-) ABGENIX INC

07-JAN-2002; 2002US-00041860.

Weber R; Gazit G, Chen F, Yang X, Feng X, Corvalan JRF, Jia X, Bezabeh B;

WPI; 2003-587119/55.

growth human New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 255; 255pp; English

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

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                                                                                                         DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                     DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                          Gaps
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                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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                                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gazit G,
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                       Anti-human PDGF-D antibody protein related sequence #23.
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                                         Score 590; DB 7;
Pred. No. 3.1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 590; DB 7;
100.0%; Pred. No. 3.1e-43;
tive 0; Mismatches 0;
                                                                          Mismatches
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                                                                                                                                                                                                                                                                           ADK18797 standard; protein; 113 AA
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                                         100.0%;
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                                                                            Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC.
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                                          Query Match
Best Local Similarity
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               Sequence 113 AA;
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The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                          antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gazit G,
                                                                                                                                                                                                        Anti-human PDGF-D antibody light chain protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 30; 255pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL25430 standard; protein; 113 AA.
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                                                                                                      ADK18606 standard; protein; 113
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587119/55.
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                                                                                                                                         ADK18606;
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ADL25430
ID ADL2
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DT 17-J
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Matches 113; Conservative

Local Similarity

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60

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61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113

1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating rephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the
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                    antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antiidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                            Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                               Lichenstein H;
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mAb 1.29 light chain variable region protein SEQ ID NO:40.
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100.0%; Pred. No. 3.1e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention
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                                                                                                                                                                                                                                                                 Gazit-Bornstein G,
                                                                                                                                                                          16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                                                   16-SEP-2002; 2002US-0411137P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113 AA;
                                                                                                                         WO2004024098-A2.
                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                       nephritis.
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 Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                           New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
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98.2%; Pred. No. 4.6e-42;
iive 1; Mismatches 0
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                                                                                                                                                                                                                                                                                              Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG65590 standard; protein; 248
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                                                                                                                06-JAN-2003; 2003WO-US000398
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Best Local Similarity 98.2
Matches 112; Conservative
                                                                                                                                                                                                                                                                                              Jia X,
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-587119/55.
                                                                                                                                                                                                                                    (ABGE-) ABGENIX INC
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WO2003057857-A2
                                                                                                                                                                                                                                                                                              Corvalan JRF,
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                                                         17-JUL-2003
                                                                                                                                                                                                                                                                                                                                Bezabeh B;
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The invention provides a human erythroid differentiation related factor (hEDRF). The hEDRF polypeptide and the encoding polymucleotide are useful for treating anemias and other erythrocyte deficiencies. The hEDRF protein is useful for producing antibodies, useful in screening assays to identify pharmaceutical compounds of interest and compounds which bind to hEDRF. The polymucleotides are useful for producing hEDRF or its related polypeptides. The antibodies are useful for separating or detecting the corresponding antigen e.g. for detection/quantitation of hEDRF in samples taken from human subjects. Quantification of hEDRF at immunohistochemical level finds value in evaluating the potential of the tissue site to contribute towards the production of new erythroid cells. The present sequence represents the amino acid sequence of an anti-hEDRF antibody e9
                                                                                               Novel human erythroid differentiation related factor and polynucleotides encoding it useful for treating anemia and other erythrocyte deficiencies and for detecting expression of the factor in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPSLIFGQGTKLEIK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable light chain; single chain antibody; scFv; human; HIb-5; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                94.2%; Score 556; DB 4; Length 248; 93.8%; Pred. No. 6.1e-40; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-platelet glycoprotein Ib human HIb-5 VL.
                 Schueler P, Harriman WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...93
-e= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .54
:e= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY95221 standard; protein; 113 AA
                                                                                                                                                                  Disclosure; Fig 4; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 93.8
nes 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                 2001-608195/70.
                 Mahoney W,
                                                                N-PSDB; AAH47762
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY95221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                 Xu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AAY95221
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Gaps

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the present sequence is that of the light chain variable region (VI) of human single chain antibody (scFv) HID-5, which is directed against contained globorotein 1b (GPID). The HID series of EcFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid a human synthetic VH and VL scFv library by 3 rounds of phagemid component of the GPID/IX/V complex on their surface, followed by a 4th component of the GPID/IX/V complex on their surface, followed by a 4th cround of selection against washed thuman platelets, and 2 final rounds in which attempts were made to displace scFv from washed platelets by complex of the GPID alpha and conclound antibody or mimotope peptide (see AAY95229). Whether displayed as surface proteins on a phagemid or secreted as free scFv by Bscherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the crown for a large and an early and an an early sequence is grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet contained in the specification are claimed. Note: The present sequence is not shown in the specification are claimed. Note: The present sequence is given in Fig 8 (see AAY95220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abzyme, antibody, immunoglobulin; infection, antimicrobial; cancer;
cytostatic; diagnostic; peptidase; light chain variable region; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPFTFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.1%; Score 555; DB 3; Length 113; 94.7%; Pred. No. 3.2e-40; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human antibody enzyme V-kappa2 VL pHVK-1 #1, SEQ:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEJ57801 standard; protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                        Claim 18; Fig 8; 89pp; English.
                                                            99WO-US025495
                                                                                                     98US-0106275P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 107; Conservative
                                                                                                                                                                                                                             WPI; 2000-365744/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
                                                                                                                                         (MILL/) MILLER
                                                            29-OCT-1999;
                                                                                                     30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-0CT-2006
                   11-MAY-2000.
                                                                                                                                                                                                                                                                                                               aggregation
                                                                                                                                                                                    Miller JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEJ57801;
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JP2006197930-A.

W0200026667-A1

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antibody with enzymatic activity using a primer based on a subgroup-
specific sequence. The antibody enzymes of the invention can be used in a
variety of fields, such as the medical industry, pharmaccutical industry,
reagent industry, medical equipment industry or food industry. The
antibody enzymes are useful in the diagnosis and treatment of medical
conditions such as cancer and various infectious dieesses, and can also
be used in biosensors and biomaterials. The antibody enzymes exhibit high
in vivo efficacy for therapeutic applications, and can be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a human antibody enzyme (abzyme) having high recognition ability and high enzyme activity. The antibody enzyme comprises a light chain encoded by a human germ line gene selected from Li22, VI-9, VI-13, VI-18, VI-22, V2-6, V2-7, V2-8, V2-13, V2-14, V3-3, A1, A2, A3, A5, A7, A10, A10, A17, A10, A19, A23, A26, A30, L14 and L22, and a heavy chain encoded by a human germ line gene selected from VH1-24, VH3-9, VH3-13, VH3-74, VH3-74, VH4-34 and VH7-81. The invention also relates to a method for producing a human antibody enzyme belonging to a particular subgroup involving selection of human lymphocyte cDNAs encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     efficiently. The present sequence represents a specifically claimed V-kappa2 light chain variable region (VL) of a human antibody enzyme having
                                                                                                                                                                                                                                                                                                                                         New human enzyme antibody consisting of light chain or heavy chain polypeptides encoded by human germ line gene e.g. L22 and VH1-24, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     listing of the specification and differs from the sequence also referred to as VL pHVK-1 (ABJ57944) which is shown in Figure 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidase activity. This sequence comprises a Ser-His-Asp (S-H-D) catalytic triad. Note: The present sequence is shown in the sequence
                                                                                                                                                                                                                                                                                                                                                                     peptides encoded by human germ line gene e.g. L22 and VH1-treatment and diagnosis of infectious diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 4; 30pp; Japanese.
                                                                      22-DEC-2005; 2005JP-00370880
                                                                                                                   22-DEC-2004; 2004JP-00372206
                                                                                                                                                                   (HIRO-) HIROSHIMA KEN
                                                                                                                                                                                                                                                                     WPI; 2006-544634/56.
N-PSDB; AEJ57800.
                                                                                                                                                                                                                   Hifumi M;
                    03-AUG-2006
                                                                                                                                                                                                                   Uda T,
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New human enzyme antibody consisting of light chain or heavy chain polypeptides encoded by human germ line gene e.g. L22 and VHI-24, useful for treatment and diagnosis of infectious diseases and cancer.

22-DEC-2004; 2004JP-00372206. 22-DEC-2005; 2005JP-00370880.

JP2006197930-A. Homo sapiens.

03-AUG-2006

(HIRO-) HIROSHIMA KEN

WPI; 2006-544634/56. Hifumi M;

Jda T,

N-PSDB; AEJ57943

Example 3; Fig 18; 30pp; Japanese

The invention relates to a human antibody enzyme (abzyme) having high recognition ability and high enzyme activity. The antibody enzyme comprises a light chain encoded by a human germ line gene selected from 122, V1-9, V1-13, V1-18, V1-22, V2-6, V2-7, V2-8, V2-13, V2-13, V3-3, A1, A2, A3, A5, A7, A10, A17, A18, A19, A23, A26, A30, L14 and L22, and a heavy chain encoded by a human germ line gene selected from VH1-24, VH3-10, VH3-13, VH3-14, VH3-13, VH3-14, VH3-13, VH3-14, VH4-34 and VH7-81. The invention also relates to a method for producing a human antibody enzyme belonging to a particular subgroup involving selection of human lymphocyte cDNAs encoding an antibody with enzymatic activity unique primer based on a subgroup-specific sequence. The antibody enzymes of the invention can be used in article and a such as the medical industry, pharmaceutical industry, reagent industry, medical equipment industry or food industry. The cativity or fields, such as the medical industry or food industry. The cativity or fields and can also conditions such as cancer and various infectious diseases, and can also be used in biosensors and biomaterials. The antibody enzymes exhibit high in vivo efficiently. The present sequence represents a V-kappa2 light chain cativity. This sequence comprises a Ser-His-Asp (S-H-D) catalytic triad. Note: The present sequence also ser-His-Asp (S-H-D) catalytic triad. Note: The present sequence as Ser-His-Asp (S-H-D) catalytic fileds. Second of the sequence also referred to as VL pHVK-1 (ABJST801) which in the sequence and the sequence of the sequence and the se

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                                                                                                                                                    DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLY-TFGQGTKLEIK 112
                                                                           1;
                                  Score 554.5; DB 10; Length 131; Pred. No. 4.2e-40;
                                                                           1; Indels
                                                                      3; Mismatches
                                  94.0%;
95.6%;
                                                                           Matches 108; Conservative
                                                      Local Similarity
Sequence 131 AA;
                                  Query Match
Best Local 6
                                                                                                                                                                                                                                                                                             RESULT 9
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16 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 75
                                         61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                           76 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLY-TFGQGTKLEIK 127
                                                                                                                                                                                                                                                 Anti-platelet glycoprotein Ib human HIb-5 VL.
                                                                                                                                                     AAY95220 standard; protein; 113 AA
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                  29-AUG-2000
                                                                                                                                                                                     AAY95220;
                                                                                                                        RESULT 10
                                                                                                                                        AAY95220
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Abzyme, antibody, immunoglobulin, infection, antimicrobial; cancer; cytostatic; diagnostic; peptidase, light chain variable region; enzyme.

Human antibody enzyme V-kappa2 VL pHVK-1 #2.

05-OCT-2006 (first entry)

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AEJ57944;

AEJ57944 standard; protein; 146 AA

AEJ57944 ID AEJ

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Gaps

1;

DB 10; Length 146; 1; Indels

Score 554.5; DB 1 Pred. No. 4.7e-40; 3; Mismatches 1

94.0%;

Ouery Match
Best Local Similarity 95.6
Matches 108; Conservative

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is shown in the sequence listing.

Sequence 146 AA;

1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA

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Variable light chain; single chain antibody; scFv; human; HIb-5;
                                                              "complementarity determining region 1"
                                                                                .61
te= "complementarity determining region 2"
                                                                                                                "complementarity determining region 3"
      glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
                                                                    .54
re= "framework region 2"
                                                                                            ...93
re= "framework region 3"
                                                note= "framework region 1"
                                                                                                                            /note= "framework region 4"
                                     location/Qualifiers
                                                                                                                                                                   99WO-US025495
                                                                                                                                                                               98US-0106275P
                                                                                                                       .113
                                                        24. .39
                                                                           note=
                                                                                        'note=
                                                                                                     /note=
                                                                                                                  'note=
                                                              'note=
                                                                                                                                                                                                                     WPI; 2000-365744/31.
                                                                                                                                                                                           (MILL/) MILLER J L.
                                                                                                                                          WO200026667-A1
                                                                                                                                                                               30-OCT-1998;
                         Homo sapiens
                                                                                                                                                                   29-OCT-1999;
                                                                                                                                                                                                                                              aggregation.
                                                                                                                                                      11-MAY-2000.
                                                                                                                                                                                                        Miller JL;
                                      Key
Region
                                                                                                          Region
                                                                                                                       Region
                                                        Region
                                                                    Region
                                                                                 Region
                                                                                              Region
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Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet

Claim 18; Fig 8; 89pp; English.

The present sequence is that of the light chain variable region (VL) of human single chain antibody (scFv) HID-5, which is directed against controlled gloppotein in (GPID). The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid a human synthetic VH and VL scFv library by 3 rounds of phagemid component of the GPID/IX/V complex on their surface, followed by a 4th crownd of selection against washed human platelets, and 2 final rounds in which mutine monoclonal antibody or minotope peptide (see ANY95229). Whether displayed as surface, from washed platelets by contract of secreted as free scFv by Escherichia coli, the HID scFv clones are secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. CF They provide a new class of antithrombotic agents, useful for the correction of platelet-dependent thrombi in diseased arteries, bypass constits, dialysis etc., and can also be used as diagnostic reagents.

Wethods of inhibiting aggregation of platelets, of binding human platelet constituted that the scFv and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human i GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed

Sequence 113 AA;

9 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA Gaps ö 93.9%; Score 554; DB 3; Length 113; 93.8%; Pred. No. 4e-40; ive 4; Mismatches 3; Indels Matches 106; Conservative Local Similarity Н Query Match

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The present invention describes a method (M1) for identifying an antipody (I) in a mammal. The autoantibody is detected by platelet autoantibody [I] in a mammal. The autoantibody is detected by platelet autoantibody plated display library from 8-1 ymphocytes obtained from the mammal, and screening the library to detect a phage that crompared in a mammal having competitive cellocompities panning. Also described: (I) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M3) platelet adhesion in a mammal; (7) treating (M3) platelet adhesion in a mammal; (8) inhibiting (M3) platelet adhesion in a mammal; (7) treating (M3) platelet autoantibody in (II) inhibiting (M3) platelet autoantibody in (II) inhibiting (M3) platelet autoantibody with a platelet activation; (10) inhibiting (M3) platelet autoantibody with a platelet; (13) a peptide that inhibits binds with an anti-platelet autoantibody with a platelet; (13) a peptide that inhibits binds with an anti-platelet autoantibody with a platelet; (13) a peptide that inhibiting platelet function; (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet aggregation, inhibiting platelet aggregation, inhibiting platelet autoantibody, or its biologically active fragment that comprises an antigen binding region derived from an H414 anti-platelet autoantibody, the kit further comprising a peptide autoantibody, or its biologically active fragment comprises an antigen binding with allogical and an instructions for use. (I) has haemostatic, anticoagliant and an instruction for use. (I) has haemostatic, anticoagliant and
                                                                                                                                                                                                                                                                                                                                               thrombus, platelet adhesion inhibition,
thrombotic thrombocytopenic purpura, platelet aggregation inhibition,
idiopathic thrombocytopenic purpura, haemostatic, anticoagulant,
                                                                                                                                                                                                                                                                                 Anti-platelet autoantibody related light chain amino acid L50 SEQ:89.
                                                                                                                                                                                                                                                                                                                       anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition;
61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                          113
                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPFTFGQGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 89; 232pp; English.
                                                                                                                                                     ADI22126 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2002; 2002US-0394352P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-2002; 2002US-0411694P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                        (first entry)
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N-PSDB; ADI22073.
                                                                                                                                                                                                                                                                                                                                                                                                                  thrombolytic; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                          22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                ADI22126;
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Claim 11; Page 77; 89pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet
and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                   1 DÍVMTÓSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRPVTFGQGTRLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable light chain; single chain antibody; scFv; human; HIb-5; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
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                                                                                                                                                                           Score 554; DB 8; Length 113;
Pred. No. 4e-40;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region
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/note= "framework region 1"
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/note= "framework region 2"
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:e= "framework region 3"
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93.8%;
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                                                                                                                                                                                                                        Matches 106; Conservative
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                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA27664
                                                                                                                                          Sequence 113 AA;
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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scFv) HID-5, which is directed against platelet glycoprotein Ib (GPID). The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID alpha component of the GPID/IX/V complex on their surface, followed by a 4th round of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scFv from washed platelets by flooding with murine monoclonal antibody or mimotope peptide (see ANY95229). Whether displayed as surface proteins on a phagemid or secreted as free scFv by Bscherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass created and also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet chibbits platelet aggregation are claimed in indiseased arteries inhibits platelet aggregation are claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                =
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93.9%; Score 554; DB 3; Length 114;
Best Local Similarity 93.8%; Pred. No. 4e-40;
Matches 106; Conservative 4; Mismatches 3; Indels
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.e= "complementarity determining region
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Le= "framework region 1"
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/note= "framework region 2"
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Best Local Similarity
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blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
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Inter peptide of human single chain antibody (scFV) HID-5, which is directed against platelet glycoprotein ID (GPID). HID-5 is composed of a directed against platelet glycoprotein ID (GPID). HID-5 is composed of a vector-derived peptide linker. The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid selection chainst transfected CHO cells expressing the GPID alpha component of the GPID/IXV complex on their surface, followed by a 4th round of selection against transfected CHO cells expressing the GPID alpha component of the GPID/IXV complex on their surface, followed by a 4th round of selection against transfected CHO cells expressing the GPID alpha component of the GPID/IXV complex on mimotope peptide (see ANY95229). Matcher displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native charapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GPID alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed
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                                                                                                                                                                                                                                                                                                                     present sequence is that of the light chain variable region (VL) plus
                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; monoclonal antibody; phospholipase A2; PLA2;
inflammatory disorder; degenerative disorder;
joint inflammatory reaction; skin inflammatory reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 554; DB 3;
Pred. No. 4.6e-40;
            /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
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                                                                                                                                                                                                                                                                                          Disclosure; Fig 8; 89pp; English.
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93.8%;
                                                                                               99WO-US025495
                                                                                                                         98US-0106275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 106; Conservative
                                                                                                                                                    ы
г.
                                                                                                                                                                                                         WPI; 2000-365744/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 131 AA;
                                                                                                                                                    (MILL/) MILLER
                                         WO200026667-A1
                                                                                              29-OCT-1999;
                                                                                                                         30-0CT-1998;
                                                                   11-MAY-2000
                                                                                                                                                                                                                                                               aggregation
                                                                                                                                                                             Miller JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP47300
 셤
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The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents the light chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; 161P2F10B antagonist; Gene therapy; antibody production; cancer; neoplasm; therapeutic; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTI--TFGQGTRLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
Alzheimer's disease; atherosclerosis; restenosis; light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee YR, Liang ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 161P2F10B antibody light chain SEQ ID NO 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 550; DB 8; 93.8%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; SEQ ID NO 215; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEK98277 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Landes GM, Haak-Frendscho M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2006; 2006WO-US012314.
                                                                                                                                                                                                                                                    02-DEC-2003; 2003WO-US038234.
                                                                                                                                                                                                                                                                                                               02-DEC-2002; 2002US-0430724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2005; 2005US-0667588P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-2006 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 93.8
nes 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC. (LEXI-) LEXICON GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-461119/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
                                                                                                                        WO2004050850-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2006105488-A2
                                                                 Homo sapiens.
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                                                                                                                                                                                      17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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The invention relates to a monoclonal antibody or its antigen binding fragment comprising an antigen binding site that binds specifically to a 161P2F10B protein, where the monoclonal antibody is 146-7.213, 1416-9.69, 1416-1.52, 1416-1.52, 1416-1.68, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416-1.61, 1416
                                                                                                                                                                                                                                                                                                                                              New monoclonal antibody that binds specifically to a 161P2F10B protein, useful for treating prostate, pancreas, bladder, kidney, colon, lung, ovary, or breast cancer.
                                                                                                                                                     SB, Challita-Eid PM, Perez-Villar JJ;
3, Morrison RK, Morrison KJM, Jia X, Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 156; 438pp; English.
20-JUL-2005; 2005US-0700975P
                                                                                                                                                     Jakobovits A, Kanner SB
Satpaev D, Raitano AB,
                                                                                                                                                                                                                                                                          WPI; 2006-680690/70.
                                                                        (AGEN-) AGENSYS INC.
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Sequence 223 AA;

1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60 Gaps 5 Length 223; 0; Indels Ouery Match 93.2%; Score 550; DB 10; Best Local Similarity 93.8%; Pred. No. 1.8e-39; Matches 106; Conservative 5; Mismatches 0; g

ð g Search completed: April 25, 2007, 04:05:21 Job time : 98.9972 secs

```
GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

April 25, 2007, 04:05:37 ; Search time 9 Seconds (without alignments) 1261.509 Million cell updates/sec

US-10-665-383-40 590 Title: Perfect score:

1 DIVMTQSPLSLPVTPGEPAS......MQALQSLMCSFGQGTKLEIK 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Ig kappa chain V r	light	Iq kappa chain - h	kappa chain V-	chain V	Ig kappa chain - h	kappa chain pr	kappa chain -	kappa	kappa chain -	Ig kappa chain V-J	kappa chain V	kappa chain -	kappa chain -	Ig kappa chain V-I	kappa chain V-	Ig kappa chain - h	Ig kappa chain V-I	Ig kappa chain V-I	Ig kappa chain V r	kappa	kappa chain	kappa chain V	anti-DNA autoantib			q kappa chain		g kappa chain
og Typing of	ΙD	S26882	S58207	S40342	S40357	S58206	S40339	K2HUGM	840356	K2HUTW	S40371	S40372	S40319	S24681	S40375	S03876	K2HUML	840321	K2HUCM	K2HUFR	S34091	S22658	F27887	B27887	PL0203	840312	B39276	938	849572	C29380
	ength DB					112 2		117 1	• •	•				100 2			112 1	130 2			87 2		112 2						-	
* Query	Match Length	92.5	92.3	92.3	92.3	6.06	7.06	90.4	90.3	86.2	86.2	86.2	85.6	84.2	82.5	81.9	81.5	78.0	77.3	76.4	75.8	75.4	75.0	74.5	74.5	74.5	٠	٠	74.4	74.4
,	Score	545.5	544.5	544.5	544.5	536.5	535	533.5	532.5	508.5	508.5	508.5	505	497	487	483.5	481	460	456	450.5	447	₹#		439.5	439.5	439.5	439.5		439	439
Result	No.	-	7	ю	4	ហ	φ	7	80	σ	10	. 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

438 74.2 114 2 \$40340 437.5 74.2 127 2 \$40323 437.5 74.2 115 2 \$38115 436.5 74.0 131 2 \$36577 436.5 74.0 133 1 2 \$36577 436.5 74.0 142 2 \$22902 435.5 74.0 142 2 \$22902 435.5 73.8 112 2 \$37119 435.5 73.8 112 2 \$41949 435.5 73.8 113 2 \$41949 435.5 73.8 113 2 \$4319 435.5 73.8 113 2 \$35750 434.5 73.6 131 2 \$35750 434.5 73.6 131 2 \$35750 433.5 73.5 112 2 \$35713	Ig kappa chain V-J	kappa		kappa	kappa	kappa	kappa	light	light	kappa	kappa	ibody		kappa	kappa
44444444444444444444444444444444444444	340	523 717	128	577	URP	902	.887	719	940	359	904	750	513	320	107
44444444444444444444444444444444444444	840	2 0	\$520	B30	K2H	S22	E27	838	B41	PTO	B34	8537	B325	S40	A318
	0.0	N C	v 64	7	-	7	7	0	7	~	~	~	8	7	7
44444444444444444444444444444444444444	114 2	115 2	219 2	131 2	133 1	142 2	112 2	112 2	113 2	118 2	131 2	112 2	131 2	96 2	112 2
	74.2 114 2	74.2 12/ 2	74.2 219 2	74.0 131 2	74.0 133 1	74.0 142 2	73.8 112 2	73.8 112 2	73.8 113 2	73.8 118 2	73.8 131 2	73.6 112 2	73.6 131 2	73.5 96 2	73.5 112 2

# ALIGNMENTS

S26882
Ig kappa chain V region (V607) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text change 20-Jun-2000
C;Accession: S26882
R; Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A; Title: Megabase inversions in the human genome as physiological events.
A; Reference number: S26882; MUID: 90370099; PMID: 2118596
A;Accession: S26882
A;Status: preliminary; translation not shown
A; Molecule type: DNA
A;Residues: 1-132 <wei></wei>
A; Cross-references: UNIPARC: UP10000116D46; EMBL: X54248; NID: 937626; PIDN: CAA3
C;Genetics:
A;Introns: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin

C; Keywords: heterotetramer; immunoglobulin F;36-115/Domain: immunoglobulin homology <IMM>

PIDN:CAA38149.1; PID

1; Gaps 7 Length 132; Indels DB 2; Score 545.5; DB 2; Pred. No. 1.2e-42; 4; Mismatches 2; Query Match 92.5%; Best Local Similarity 93.8%; Matches 106; Conservative

1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60 80 21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 셤 ઠ

SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPQ-TFGQGTKVEIK 132 SGVPDRFSGSGSGTDFTLKISRVBADDVGVYYCMQALQSLMCSFGQGTKLEIK 113 19 81 ð 엄

RESULT

Signate thain V region anti-F(ab')2 - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: SS8207
A;Reference to the EMEL Data Library, July 1995
A;Reference number: SS8206
C;Residues: 1-112 <WEL>
A;Gross: Teferences: UNIPARC: UPI0000116253; EMBL: X89056; NID:9929642; PIDN: CAA61443.1; PI]
C;Supwords: immunoglobulin homology <a href="mailto:keywords: immunoglobulin">k,fc-95/Domain: immunoglobulin | k,fc-95/Domain: immunoglobulin | k,fc

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A;Cross-references: UNIPARC:UP10000116252; EMBL:X89054; NID:9929640; PIDN:CAA61441.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UP10000116159; EMBL:X72449; NID:9441366; PIDN:CAA51117.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                      C;Accession: S58206
R;Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, Bubmitted to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region A;Reference number: S58206
A;Accession: S58206
                                                                                                                                                            $58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Uan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHINGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: $40339
R;Klain, R.; Jachau, H.G.
Birtlain, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40339
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQALQP--WTFGQGTKVEIK 126
61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 535; DB 2; Length 126;
Pred. No. 1e-41;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V-II region (GM607) - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 6.7e-42;
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P;16-95/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 92.0%;
Matches 104; Conservative
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40342
R;Klein, R: J Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                        1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                     Gaps
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                                                                                                                                                                                                                                                                                 SGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT-PWTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                               Length 112;
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                               DB 2;
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93.8%; Pred. No. 1.5e-42;
cive 4; Mismatches 2
                               Score 544.5; DB 2
Pred. No. 1.3e-42;
                                                                                  4; Mismatches
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A; Cross-references: UNIPROT:QBNEKO; UNI
C; Superfamily: immunoglobulin homology
C; Keywords: heterotetramer; immunoglobu
F; 36-115/Domain: immunoglobulin homology
                            92.3%;
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Best Local Similarity 93.8<sup>1</sup>
Matches 106; Conservative
                                                                                  Matches 106; Conservative
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Best Local Similarity 93.8
Matches 106; Conservative
                                                         Best Local Similarity
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A;Status: preliminar
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from a case of primary amylo
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R; Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, B.F.; Glenner, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A; Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with A; Reference number: A92764; MUID:73166638; PMID:4700495
A; Contents: amyloid protein Tew
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Accession: 840371
A;Accession: S40371
A;Accession: S40371
A;Accession: S40371
A;Accession: S40371
A;Accession: Jamunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-92/Domain: immunoglobulin homology <IMM>
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      C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A90370; A92764; A01888
R;Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
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;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                         A;Title: Amino acid sequence of a kappa Bence Jones protein A;Reference number: A90370; MUID:74148480; PMID:4596149 A;Contents: Bence Jones protein Tew A;Accession: A90370
                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: P01617; UNIPARC: UPI000012E157
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Local Similarity 86.7%; Pred. No. 2.3e-39;
hes 98; Conservative 11; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A92764
A,Molecule type: protein
A,Residues: 1-27 <TER>A,Cross-references: UNIPARC:UP10000173706
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A;Cross-references: GDB:136265
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                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-113 < PUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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S40371
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01889; B24452
R;Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A;Title: Contribution of human V-kappall germ-line genes to light-chain diversity.
A;Reference number: A01889; MUID:84191506; PMID:6325927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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840356
840356
19 kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840356
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bir. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F;5-117/Product: 1g kappa chain V-II region (GM607) #status predicted <MAT>
F;20-99/Domain: immunoglobulin homology cTMM>
F;27-97/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                              A;Accession: A01889
A;Molecule type: mRNA
A;Residues: 1-17 < KLO>
A;Cross-references: UNIPROT:P06309; UNIPARC:UPI000012E158
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin;25-104/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S40312; MUID: 94080891; PMID: 8258341 A; Accession: S40356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 533.5; DB 1;
Pred. No. 1.3e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104; Conservative
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A; Residues: 1-125 <KLE>
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RESULT 9

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A;Cross-references: UNIPARC:UPI00001160El; EMBL:X67904; NID:g33435; PIDN:CAA48102.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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R;Ferri, G;; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989 Biochim. Biophys. Acta 995, 103-108, 188pa II Inc, a new amyloid immunoglobulin. A;Reference number: S03876; MUID:89194238; PMID:2495028
A;Accession: S03876
A;Molecule type: protein
A;Residues: 1-124 <FER>
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S24681
A;Reference number: S24679
A;Reference number: S24679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-II region (Inc) - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHRYGYNYLDWYLQKPGQSPQLLIYLGSNRA
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R; Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A; Tile: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: $40312; MUID:94080891; PMID:8258341
A; Accession: $40375
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-114 < KLE>
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84.2%; Score 497; DB 2;
Best Local Similarity 96.0%; Pred. No. 2.3e-38;
Matches 95; Conservative 2; Mismatches 2;
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S03876
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C.Species: Homo sapiens (man)
C.Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Accession: $40319
F.Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A.; Fitle: Expressed human immunoglobulin chi genes and their hypermutation.
A.; Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                     RESULT 11
S40372
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40372
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference numbor: S40312; MUID:94080891; PMID:8258341
A;Reference numbor: translation not shown
A;Residues: 1-131 <KLE>
A;Residues: 1-131 <KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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C;Keywords: heterotetramer; immunoglobulin
F;26-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 508.5; DB 2; Length Pred. No. 2.7e-39; 6; Mismatches 6; Indels
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A;Cross-references: UNIPARC:UP1000017679D
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <1MM>
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8888	Cop	Copyrighted Distributed	d by th	e UniPr	ot c	by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License	w.uniprot.org/terms oberiva License
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
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PIR, S34091; S34091.
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PIR, S40357; S40357.
HSSP; P01834; 1172.
SMR, Q9NEKO; 21-237.
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Homo sapiens (Human).
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RM Strausberg N.L.; Peingold E.A.; Grouse L.H., Derge J.G.;

RA Strausberg N.L.; Peingold E.A.; Grouse L.H., Derge J.G.;

RA Altasiner R.D.; Collins F.S.; Wagner L., Shemmen C.M.; Schuler G.D.;

RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

B. Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

RA Brownstein M.J.; Uddin T.B.; Tasmer A.A.; Rubin G.M.; Hong L.;

RA Rahas S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

RA Rahas S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

RA Richards S., Worley K.C.; Hale S.; Garcia A.M.; Gubbs R.A.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Villalon D.K.; Muzny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.;

Rahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;

RA Rodriguez A.C.; Grimwood J.; Schwutz J.; Myers R.M.;

Rakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

RA "Generation and initial analysis of more than 15,000 full-length human P.M. P.M.
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Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
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"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                         DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini,
Catarrhini, Hominidae, Homo.
                                                                                            1;
                                              Score 533.5; DB 1; Length 117; Pred. No. 2.7e-49;
                                                                                            4; Indels
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Director MGC Project;
Submitted (JUN-2002) to the BMBL/GenBank/DDBJ databases.
12664 MW; 92C57DC719E558B1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002, integrated into UniProtKB/TrEMBL. 01-OCT-2002, sequence version 1. 27-JUN-2006, entry version 30.
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Eur. J. Immunol. 22:1561-1565(1992).
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Eur. J. Immunol. 23:391-397(1993).
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                                              90.4%;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
  117 AA;
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGKV1-5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=IGKV1-5;
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                                                                                                                                                                                                                                       61
  SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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GO; GO:0016020; C:membrane; IEA.
GO; GO:00106020; C:membrane; IEA.
GO; GO:00101062 : P:MHC Class I receptor activity; IEA.
GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
GO; GO:0019885; P:antigen processing, endogenous antigen via . .; IEA.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR001597; Ig-12ke.
InterPro; IPR001599; Ig-8ub.
InterPro; IPR001599; Ig-8ub.
InterPro; IPR001596; Ig-V-set.
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                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
MEDLINE=94080891; PubMed=8258341;
Klein R., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Fur. J. Immunol. 23:3248-3262(1993).
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVMTQSPLSLPVTPGBPASISCRSSQSLLHSDGYNYLDWYLQWPGQSPQLIYLGSNRA
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%; Score 532.5; DB 2; Length 90.3%; Pred. No. 8.5e-49; ive 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SEQUENCE 239 AA; 26024 MW; FSEZ0AD3B0552COA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFIH6;
05-UL-2004, integrated into UniProtKB/TrEMBL.
05-UL-2004, sequence version 1.
27-UW-2006, entry version 21.
IGKVL-5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                 BC030814; AAH30814.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEPIHE_HUMAN PRELIMINARY; PRT;
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Ig kappa chain V-II region TEW.
       HSSP; D0837; 1835.

R HSSP; D0837; 1835.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:imembrane; IEA.

GO; GO:001906; F:MHC class I receptor activity; IEA.

GO; GO:001988; P:antigen processing, endogenous antigen; IEA.

R GO; GO:001988; P:antigen processing, endogenous antigen via . . .; IEA.

InterPro; IPR00359; Ig_Cl-set.

R InterPro; IPR00359; Ig_Cl-set.

R InterPro; IPR00359; Ig_WHC.

R InterPro; IPR00359; Ig_WhC.

R InterPro; IPR00359; Ig_WhC.

R InterPro; IPR00359; Ig_W-set.

R Pfam; PF07684; Cl-set; I.

R Pfam; PF07684; Cl-set; I.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
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91.2%; Pred. No. 9.7e-49;
ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SW00409; IG; 1.
SWART; SW00409; IG; 1.
SWART; SW00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Immunoglobulin; Memain; Memain; Repeat; Transmembrane.
SEQUENCE 240 AA; 26234 WW; 188D4DD8BB781EC4 CRC64;
                                                                                                                                                                                                                                                   Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC034142; AAH34142.1; -; mRNA
                                                                                                                                                                                                                                   and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 103; Conservative
                                                                                                                                                                                                                                                                                             TISSUE=Lung;
Director MGC Project;
                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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     셤
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integrated into UniProtKB/Swiss-Prot.

sequence version 1.

KV2D HUMAN P01617; 21-JUL-1986; 21-JUL-1986; 30-MAY-2006;

TAPAT P

entry version 47

113 AA.

STANDARD;

RESULT 4 KV2D\_HUMAN

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Distributed under the Creative Commons Attribution-NoDerivs License
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.
                                                                                                                                                 MEDLINE-74148480; PubMed-4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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R GO; GO: 0005823; F: antigen binding; NAS.

R GO; GO: 0006955; P: immune response; NAS.

R GO; GO: 0006955; P: immune response; NAS.

R InterPro; IPR001310; Ig-like.

R InterPro; IPR013106; Ig-V-set.

R InterPro; IPR013106; Ig-V-set.

R Pfan; PF07686; V-set; 1.

R SMART; SM00409; IG; 1.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

R MAPQ10id; Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.

T CHAIN 1 >113 Ig Asppa chain V-II region TEW.
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                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW)
                                                                                                                                PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW).
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39
54
61
102
112
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                                                                                                                                                                                                              primary amyloidosis.";
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SMR; P01617; 1-111.
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                                                                                        NCBI_TaxID=9606;
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KV2C\_HUMAN

RESULT 5

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PROTEIN SEQUENCE.
MEDLINE=68242259; PubMed=5586923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Best Local Similarity
Matches 93; Conserv
                                                        NCBI_TaxID=9606;
                                                                                                                         Hilschmann N.;
                                                                                                                                                                                                                                   Hilschmann N.;
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P01615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SW00406; IGv; 1.
PROSITE; PSSOBS5; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                Dreyer W.J., Gray W.R., Hood L.E.;
"The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-i- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-i- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 SGVPNRFSGSGSGTBFTLKISRVZAZBVGVYYCMQALQTPL-TFGGGTNVEIK 111
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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Framework-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12057 MW; E5B22E2FA7ABE481 CRC64;
                                                                         21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 21-JUL-1986, sequence version 1. 30-MAY-2006, entry version 41. 19 kappa chin V-II region MIL. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986, integrated into UniProtKB/Swiss-Prot. 2-J-UL-1986, sequence version 1. 30-MAY-2006, entry version 45. Ig kappa chain V-II region Cum.
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                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, Q99M37, 1191.
SWR, P01616, 1-110.
InterPro; IPR07110, Ig-like.
InterPro; IPR03199; Ig_sub.
InterPro; IPR013106; Ig_V.set.
InterPro; IPR003596; Ig_V.set_sub.
Pfam, PP07686; V-set, 1.
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80.5%;
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Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                             STANDARD;
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101
111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA;
                                                                                                                                                                                                                                     PROTEIN SEQUENCE.
                                                                                                                                                                                                       NCBI_TaxID=9606;
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P01614;
                                             HUMAN
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InterPro; IPR001559; Ig sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR001556; Ig_V-set_sub.
Pfam; PF07686; V-set; 1.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-206(1969).
Naturwissenschaften 56:195-206(1969).
-!- MISCELLANBOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANBOUS: This is a Bence-Jones protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ASGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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By similarity.
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                                                                                                                                                                                                                                                                                                      Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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81.6%; Pred. No. 6.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0005576; C:extracellular region, NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE REVISION TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                            EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
PIR; A01890; K2HURP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-4.
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III.";
Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
14707 MW;
                                                                                                                                                                                                                                                                                                        PS50835, IG LIKE; 1.
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Best Local Similarity 76....
-has 86; Conservative
                                                                                                                                                                                                                                                    Pfam; PF07686; V-set; 1.
SMART; SM0409; IG. 1.
SMART; SM00406; IG.; 1.
PROSITE; PS50835: IG 17777
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59
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133 AA;
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NUCLEOTIDE SEQUENCE.
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                                   Riesen W.P., Jacon J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Blochemistry 15:3829-383(1976).
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ammalia, Eutheria, Buarchontoglires, Primates, Haplorrhini,
Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.4%; Score 450.5; DB 1; Length 113; 77.0%; Pred. No. 2.4e-40; live 12; Mismatches 13; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-II region FR. /FTId=PRO 0000059759.
Framework-1.
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                                                                                                                                                                                       HSSP, Q99M37; 1191.

SMR; P01615; 1-109.

GO; GO:0003823; E:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
InterPro; IRRO7110; Ig-1ke.
InterPro; IRR003106; Ig-V-set.
InterPro; IRR003599; Ig-W-set.
InterPro; IRR003599; Ig-V-set.
InterPro; IRR003599; Ig-V-set.
SMART; SM00409; IG; I.
PROSITE; PS50835; IG-IKE; I.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988, integrated into UniProtKB/Swiss-Prot. 01-JAN-1988, sequence version 1. 30-MAY-2006, entry version 43. Ig kappa chain V-II region RPMI 6410 precursor. Homo sapiens (Human).
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         PROTEIN SEQUENCE.
MEDLINE=76253627; PubMed=821524;
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39
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102
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Best Local &
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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/FTId=PRO_000015173.
Framework-1.
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Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
Brinkmann U., Pai L.H., maingle-chain immunotoxin that causes complete regression of a human carcinoma in mice.";
Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 436.5; DB 1; Length 133; 76.1%; Pred. No. 9.4e-39; ive 12; Mismatches 14; Indels 1.
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HSSP, Q99M37, 1191.

SMR; P06310; 21-133.

Ensembl; ENSG00000173758; Homo sapiens.
LinkHub; P06310; -...
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005555; P:immune response; NAS.
InterPro; IPR003110; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR013106; Ig-V-set.
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Distributed under the Creative Commons Attribution-NoDerivs License
see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;
Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
Exlandsson f. the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                          1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                         Gaps
         Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                           196 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQG-SHVPFTFGSGTKLEIK 247
                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                        1;
                                                                                                                                                                    Length 248;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;
                                                                                                                                                 248 AA; 26634 MW; 7A3759B43E570950 CRC64;
                                                                                                                                                                    74.0%; Score 436.5; DB 2; 75.2%; Pred. No. 2e-38;
                                                                                                                                                                                                                                                                                                                                         15-MAR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                    15-MAR-2005, sequence version 1.
11-UUL-2006, entry version 8.
Kappa light chain variable region (Fragment)
Mame=IgG1 anti-TS1 VL,
                                                                                                                                                                                        12; Mismatches
Copyrighted by the UniProt Consortium,
                                   SMX; Q65207; 4-247.
InterPro; IPR007110; Ig-like.
InterPro; IPR01359; Ig-sub.
InterPro; IPR013596; Ig-v-set.
InterPro; IPR013106; Ig-V-set.
Efam; PP07686; V-set; 2.
SMART; SM00406; IG; 2.
PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ884575; CAI56337.1; -; mRNA.
SMR; Q5F210; 1-115.
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig_sub.
InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set_sub.
                          EMBL; S57990; AAB19971.2; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                             Local Similarity 75.2%
Les 85; Conservative
                                                                                                                            Immunoglobulin domain.
NON TER 248 248
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erlandsson A.;
                                                                                                                                                                                                                                                                                                                     QSF2IO_MOUSE
                                                                                                                                                SEQUENCE
                                                                                                                                                                     Query Match
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg K.L., Feligold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chencra A., Schein J.E., Jones S.J.M., Marra M.A.;
Chentertion and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                  SGVPDRPSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPYTFGGGTKLEMK 113
                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92201291; PubMed=1551402;
Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
Thiebe R., Zocher I., Zachau H.G.;
"The human immunoglobulin kappa locus. Characterization of the
                                                                        .;
0
       Length 115;
                                                                        17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
Query Match 73.9%; Score 436; DB 2; Best Local Similarity 75.2%; Pred. No. 8.9e-39; Matches 85; Conservative 11; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Immunol. 22:1023-1029(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nephritis-associated idiotype.";
Nucleic Acids Res. 20:2601-0(1992)
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MEDLINE=92285150; PubMed=1598223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002, sequence version 1.
27-JUN-2006, entry version 29.
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 duplicated A regions."
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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QETCDO;
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.8%; Scott 1.18-Best Local Similarity 75.2%; Pred. No. 1.18-Matches 85; Conservative 12; Mismatches
                     Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMR; QBTCD0; 21-237.

R GO; GO: 0016021; C:integral to membrane; IEA.

R GO; GO: 0016020; C:membrane; IEA.

R GO; GO: 0016020; C:membrane; IEA.

R GO; GO: 0016020; C:membrane; IEA.

R GO; GO: 0018081; P:mHC class I receptor activity; IEA.

R GO; GO: 0018085; P:antigen processing, endogenous antigen via . . ; IEA.

InterPro; IPR001309; Ig_CI-set.

R InterPro; IPR001306; Ig_MHC.

R InterPro; IPR001306; Ig_MHC.

R InterPro; IPR001306; Ig_WHC.

R InterPro; IPR001306; Ig_Wet.

R InterPro; IPR001306; Ig_V-set.

R InterPro; IPR001306; Ig_V-set.

R InterPro; IPR001306; Ig_V-set.

R Pfam; PF07654; CI-set; I.

R Pfam; PF07656; V-set; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
MEDLINE=94080891; PubMed=8258341;
KTein K., Jaenichen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWPQQRPGQSPRRLIYKVSNRD
                                                                                                                             Wagner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTH-WPSTFGQGTKLEIK 132
                                                                                                                                                                                      somatic mutation.";
Eur. J. Immunol. 23:391-397(1993).
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00407; IGC1; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PSC00315; IG LIKE; 2.
PROSITE; PSC00290; IG MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 72.8%; Score 429.5; DB 2; Length 239; Local Similarity 74.3%; Pred. No. 1.1e-37; hes 84; Conservative 14; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                           EMBL; BC022362; AAH22362.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q58EU8 MOUSE PRELIMINARY; PRT;
Q58EU8;
                                                                                           NUCLEOTIDE SEQUENCE.
MEDLINE=93170387; PubMed=8436174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2005, sequence version 1.
25-JUL-2006, entry version 19.
Igk-C protein.
Name=Igk-C;
                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, S40374; S40374.
PIR, S42267; S42267.
PIR, S42268; S42268.
HSSP, P01834; II7Z.
SMR, Q8TCD0; 21-237.
                                                                                                                                                                                                                                                                                                                                                          PIR; S22658; S22658.
PIR; S34095; S34095.
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RRYRY RYYRY RRYRY RYRY RRYRY R

RESULT 12 028EUB MOU 1D QEBEU AC QEBEU DT 26-AP DT 26-AP DT 25-AU DE IGK-C GN Name= OG Name CC

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R EMBL; BC091750; AAH91750.1; -; mRNA.

R G0; G0:0016021; C:integral to membrane; IEA.

RG; G0:0016021; C:integral to membrane; IEA.

RG; G0:0016020; C:membrane; IEA.

RG; G0:0010106; F:MHC class I receptor activity; IEA.

RG; G0:0019883; P:antigen processing, endogenous antigen; IEA.

RG; G0:0019885; P:antigen processing, endogenous antigen via . .; IEA.

RR G0; G0:0019885; P:antigen processing, endogenous antigen via . .; IEA.

RR InterPro; IPR003507; Ig\_C1-set.

R InterPro; IPR003509; Ig\_MLC.

R InterPro; IPR003106; Ig\_Wet.

R InterPro; IRR003599; Ig\_wet.

R InterPro; IRR003599; Ig\_wet.

R PR003564; C1-set; I.

R Pfam; PF07684; C1-set; I. NOTICE STOCKEN IN TISSUE-Mammary tumor metastatized to lung.

NUTRAIN-EZECH II; TISSUE-Mammary tumor metastatized to lung.

MEDLINE-238827; PubMed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Alsenis R.E., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alsenis R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rownstein M.J., WcEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha J., Melton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodreration and initial analysis of more than 15,000 full-length human 9 80 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License 21 DVVWTQTPLTLSVTIGQPASISCKSSQSLLHSNGKTYLNWLLQRPGQSPKLLIYLVSKLE 1 DIVMTOSPLSLPVTPGEPASISCRSSOSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA Gaps 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113 PROSITE; PS50835; IG\_LIKE; 2. PROSITE; PS00290; IG\_MHC; UNKNOWN 1. Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat; STRAIN=CZECH II; TISSUB=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.; ï 72.8%; Score 429.5; DB 2; Length 239; 75.2%; Pred. No. 1.1e-37; 15; Indels Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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239 AA; 26246 MW; CD7313DDFFD358B3 CRC64;
Transmembrane
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                      SEQUENCE
                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Ehat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Ehat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
And J. Helton E., Ketteman M., Radan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                    239 AA
                                                                                 QGP491 HUMAN PRELIMINARY; PRT;
Q6P491;
                                                                                                                                             05-JUL-2004, sequence version 1. 27-JUN-2006, entry version 22. Hypothetical protein LOC651928.
                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
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                                                                                                                                                                                                              Name=LOC651928;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE
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                                                              HUMAN
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                                     RESULT 13

OS 491 HUM

ID 06491 HUM

ID DT 06-101

DE 06749

DE 06749

DE 06749

OC 06749

OC 06749

OC MAMMEN

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                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
18-APR-2006, entry version 2.
Myosin-reactive immunoglobulin light chain variable region (Fragment).
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Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
                                                                                                                                                                      21 DIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQRPGQPPRLLIYKISNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE-91170387; PubMed=8416174;
MEDLINE-91170387; PubMed=8436174;
MEDLINE-91170387; PubMed=8436174;
Magner S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=92352481; PubMed=1322670;
Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W.
Gaskin F., Fu S.M.;
                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                            81 SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQ-VSHFPRTFGQGTRVBIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A rheumatoid factor from a normal individual encoded by VH2 and V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).

Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
      Length 239;
                                                                 Indels
                                                                    16;
      DB 2;
ch 72.6%; Score 428.5; DB 2, 1 Similarity 75.2%; Pred. No. 1.4e-37; 85; Conservative 11; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
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Eur. J. Immunol. 22:1561-1565(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kappa II gene segments.";
Arthritis Rheum. 35:900-904(1992)
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InterPro; IPR003599; Ig sub:
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PIR; S34094; S34094.
PIR; S34095; S34095.
HSSP; P01625; 1LVE.
SMR; Q9UL80; 1-114.
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PIR; S23638; S23638.
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          somatic mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
Q9ULBO HUMAN
ID Q9ULBO HUMAN
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
21-JUL-1986, sequence version 1.
30-MAY-2006, entry version 40.
Ig kappa chain V-II region 26-10.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Buarchontcolires; Glires; Rodentia; Sciurognathi;
Muroidea; Muriae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Blochemistry 22:1153-1158(1983).
-!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
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R Ensembl; ENSWIGSG0000055115; Mus musculus.

R InterPro; IPR0013599; Ig_sub.

R InterPro; IPR013106; Ig_V-set.

R InterPro; IPR013596; Ig_V-set.

R Pfam; PF07686; V-set; I.

R SWART; SM00406; IG; I.

R SWART; SM00406; IG; I.

R PROSITE; PS50835; IG_LIKE; I.

R PROSITE; PS50835; IG_LIKE; I.

R PROSITE; PS50835; IG_LIKE; I.

R PROSITE; IR PROCEDIAL SEQUENCING; IR Direct protein sequencing; Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Monoclonal antibody.

I CHAIN I > 113 II region 26-10.
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                                                                                                                                                                                                                                                                                                                  Length 114;
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Framework-4.
                                                                                                                                                                                                                                                                                                            ch 72.4%; Score 427; DB 2; Length 11. Similarity 74.3%; Pred. No. 8.2e-38; 84; Conservative 12; Mismatches 17; Indels
                                                                                                                                                                                                                            114 114
114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
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InterPro; IPR013106; Ig_V-set.
InterPro; IPR003596; Ig_V-set_sub.
Pfam; PF07686; V-set; 1.
SWART; SW00409; IG; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
IGMULOGIODULIN domain.
NON TER 114 114
SEQÜENCE 114 AA; 12775 MW; 070B3
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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STRAIN=A/J;
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RV2G MOUSE

ID KV2G MOUSE

ID T21-JUL.

DT 21-JUL.

DT 21-JUL.

DT 21-JUL.

DT 30-MATH

OC BUKATY,

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                                                                                                                                                1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                            Gaps
                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTH-VPPTFGGGTKLEIK 112
                                                                                                            1;
                                                                         DB 1; Length 113;
                                                                       Query Match 72.3%; Score 426.5; DB 1; Length Best Local Similarity 74.3%; Pred. No. 9.2e-38; Matches 84; Conservative 13; Mismatches 15; Indels
                                     113 AA; 12273 MW; F9F39CE949A84C2A CRC64;
 By similarity.
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Search completed: April 25, 2007, 04:06:36 Job time : 77.9294 secs

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92.8%;
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-769B-15
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Sequence 178, App
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696.311 Million cell updates/sec
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1 DIVMTQSPLSLPVTPGEPAS......MQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       JEMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Biocceleration Ltd
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US-09-490-153-15

US-09-490-153-15

US-09-254-15

US-09-254-15

US-08-313-39BA-49

US-08-31-39BA-49

US-08-731-39BA-49

US-08-75-169B-29

US-09-025-769B-29

US-09-025-769B-29

US-09-025-769B-29

US-09-490-070A-29

US-09-490-153-29

US-09-490-153-29

US-09-490-153-178

US-09-490-153-178

US-09-490-324-178

US-09-490-324-178
                                                                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     650591 segs, 87530628 residues
 version -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                          US-10-665-383-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547.5
5447.5
5447.5
5533.5
5533.5
5531.5
5521.5
5521.5
5521.5
5521.5
5521.5
5521.5
5521.5
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5521.5
5521.5
5521.5
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                                                                                          Run on:
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Sequence 15,
Sequence Sequence S
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Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ADG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James P. Haley, Jr., Esq.
REGISTRANION NUMBER: 27,794
REFERENCE/DOCKT NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHOME: (212)596-9000
TELEPHOME: (212)596-9000
TELEPHOME: CIADAGTICS:
TELEPHOME: IBM NOBER: SEQUENCE CHARACTERISTICS:
TELEPHOME: (212)596-9000
TELEPHOME: AMAGTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plucekthun, Andreas
APPLICANT: Plucekthun, Andreas
NUMBER OF SEQUENCES: 373
                        US-10-2130-613A-71
US-09-20-214-30
US-09-24-30
US-09-448-798-30
US-08-478-039-88
US-10-000-986-8
US-10-000-986-8
US-10-000-9868-8
US-10-000-9868-8
US-10-000-9868-8
US-08-477-4848-151
US-08-107-6690-15
US-08-177-788A-15
US-08-177-788A-15
US-08-177-788A-15
US-08-477-5318-151
US-08-477-5318-151
US-08-477-5318-151
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09025769B Patent No. 6300064 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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Score 547.5; DB 2; Length 113; Pred. No. 1.3e-46;

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JS-09-490-153-15
 RESULT 3
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                                   DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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 1; Gaps
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Sequence 15, Application US/09490070A

Sequence 15, Application US/09490070A

Sequence 15, Application US/09490070A

SENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE Colin & Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe

Walther & McAuliffe

STREET: 1666 K Street, N.W., Suite 300
                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT-PYTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.8%; Score 547.5; DB 2; Length 113; 94.7%; Pred. No. 1.3e-46; tive 3; Mismatches 2; Indels 1.
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.7°
Matches 107, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
 Matches 107; Conservative
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1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.8%; Score 547.5; DB 2; Best Local Similarity 94.7%; Pred. No. 1.3e-46; Matches 107; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, TOWN APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153 FILING DATE: 24-Jan-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-490-153-15
Sequence 15, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-490-324-15
; Sequence 15, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappik, Achim Pack, Peter Ilag, Vic Ge, Liming Moroney, Simon
                                                                       APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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DIVMTQSPLSLPVTPGEPASISCRSSQSLLHNNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT-PYTFGQGTKLEIK 112
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                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                          Score 544.5; DB 2;
Pred. No. 2.6e-46;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paeten, Ira
APPLICANT: Willingham, Mark
APPLICANT: Bringerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
PRIOR APPLICATION NUMBER: 231472/1996
PRIOR FILING DATE: 1996-09-02
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                             92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.8<sup>1</sup>
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SI.
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Market P
CITY: San Francisco
STATE: California
                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                             US-09-254-180C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                           TYPE: PRT
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APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: WARNA, Motomi
APPLICANT: NAKATA, Motomi
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand or CURRENT APPLICATION NUMBER: US/09/254,180C
CURRENT APPLICATION NUMBER: PCT/JP97/02983
PRIOR APPLICATION NUMBER: PCT/JP97/02983
PRIOR APPLICATION NUMBER: 271546/1996
PRIOR FILING DATE: 1996-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                       TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPFRANE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-3n-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 547.5; DB 2; Length :
Pred. No. 1.3e-46;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-PEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
  Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09254180C
Patent No. 6777540
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.8%;
Best Local Similarity 94.7%;
Matches 107; Conservative
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: OKUMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-254-180C-9
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RESULT 8
US-08-759-804A-49
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOGLOTPQ-TFGOGTKVEIK 112
                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                   1;
                                                                                                                                  90.4%; Score 533.5; DB 1; Length 112; 92.0%; Pred. No. 3.1e-45; ive 4; Mismatches 4; Indels 1
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Variable Light chain (V-L)"
                                            /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION NUMBER: US 07/767,331
APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
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US-08-31-397B-49
Sequence 49, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 112 amino acids
amino acid
                                                                                                                               Query Match
Best Local Similarity 92.0%
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                     LOCATION: 1..112
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 1..112
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-331-397B-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                     US-08-331-398A-49
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1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA
                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQ-TFGQGTKVEIK 112
                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                      1;
90.4%; Score 533.5; DB 1; Length 112; 92.0%; Pred. No. 3.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments.
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-DEC-1996
CLASSIFICATION TOWNER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION TOWNER: US/08/331,398
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US/07/67,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US/07/67,331
FILING DATE: 12-OCT-1990
ATTONNEY/AGENT: 12-OCT-1990
ATTONNEY/AGENT: 11PPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.4%; Score 533.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/08759804A Patent No. 5990296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
RELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids
                            Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.112
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
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Sequence 29, Application US/09025769B Patent No. 6300064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patent Tr Professional Patent Professional Profe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim APPLICANT: Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 92.0 Matches 104; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-330-613A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 112
                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                 61
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APPLICANT: UNG, SUL-Hee
APPLICANT: LEE, BYLINGKOOK
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
CORRESPONDENCES:
ADDRESSEE: TOWNSEND AND TOWNSEND KNOWN AND TOWN AND T
                                                                                                                                          1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCMQGLQTPQ-TFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVBADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 3.1e-45;
4; Mismatches 4; Indels 1
                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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OTHER INFORMATION: /note= "Human 1gM GM607 VL region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 194105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
    Pred. No. 3.1e-45;
4; Mismatches 4
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REPERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTOMACY AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
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BENHAR, Itai
PADLAN, Eduardo A.
92.08;
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Best Local Similarity 92.0%;
Matches 104; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                               104; Conservative
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MOLECULE TYPE: peptide
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Best Local Similarity
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US-09-227-693-49
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                                               Matches
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                                 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN CURRENT APPLICATION NUMBER: US/10/330,613A CURRENT PILING DATE: 2002-12-26 PRIOR APPLICATION NUMBER: 60/346299 PRIOR PILING DATE: 2001-12-18 NUMBER OF SEQ. ID NOS: 90 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30 (EPO)
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APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP 95 11 3021.0
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APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
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RESULT 13
US-09-490-070A-29
US-09-025-769B-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQH-YTTPPFFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PRIOR APPLICATION DATA:
APPLICATION DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/09025769B
Sequence 45, Application US/09025769B
Setent No. 6300064
GENERAL INFORMATION:
APPLICANT: Rangpik, Achim
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Morroney, Siming
APPLICANT: Morroney, Siming
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.4%; Score 521.5; DB 2; Best Local Similarity 90.3%; Pred. No. 4.8e-44; Matches 102; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: BP 95 11 3021.0
PILING DATE: 19 B-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                  NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPRENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR ESQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
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  ATTORNEY/AGENT INFORMATION:
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amino acid
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                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-025-769B-29
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                                                                                                                                                                                                                                                                              linear
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TOPOLOGY:
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1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGTNYLDWYLQKPGQSPQLLIYLGSNRA 60
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                                                 Gaps
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                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQH-YTTPPTFGQGTKVEIK 112
                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ge, Liming
Moroney, Simon
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
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COMPUTER READABLE FORM:
COMPUTER: Ploppy disk
COMPUTER: 1BM PC compatible
COMPUTER: Patent: PC-DOS/MS-DOS
SOFTWARE: Patent: Release #1.0, Version #1.30 (BPO)
    Length 114;
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                                                 Indels
Score 521.5; DB 2;
Pred. No. 4.8e-44;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-29
                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
    88.4%;
  Query Match
Best Local Similarity 90.3
Matches 102; Conservative
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COUNTRY: USA
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61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQH-YTTPPTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 18 PC compatible
COMPUTER: 18 PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COLIN G. SANGETCOK, ESQ.
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTY: USA ZIP: 20006 COMPUTER READABLE FORM:
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                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45
                                                                                                                          Sequence 45, Application US/09490070A
Patent No. 6696248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 912-2000
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Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 912-2
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                    RESULT 14
US-09-490-070A-45
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US-09-490-153-29
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                                                                                                                                                             c/o Fish & Neave
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                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30 (EPO)
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.4%; Score 521.5; DB 2; Best Local Similarity 90.3%; Pred. No. 4.8e-44; Matches 102; Conservative 4; Mismatches 6;
                                                                                                                                                        ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-09-490-153-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 25, 2007, 04:08:32 Job time : 15.2048 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAR: (212) 596-9000
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   COUNTRY: USA
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Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 212, Appl Sequence 212, Appl Sequence 210, Appl Sequence 210, Appl Sequence 210, Appl Sequence 123, Appli Sequence 4, Appli Sequence 4, Appli Sequence 113, Appli Sequence 145, Appli Sequence 146, Appli Sequence 146, Appli Sequence 167, Appli Sequence 167, Appli

Appli Appli Appli Appli Appli Appli

Sequence ( Sequence ( Sequence (

Perfect score:

Seguence:

OM protein

Scoring table:

Searched:

Database

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1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JULY COLUMN NO. US20030157109A1

SEQUENCE 30. Application US/10041860

Publication No. US20030157109A1

SERNERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

TITLE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX. 051A

CURRENT APPLICATION UNMERS: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 113
                                       US-10-388-389-6
US-10-703-713-6
US-10-704-703-6
US-10-232-030-6
US-10-292-088-28
US-10-292-088-28
US-10-292-088-32
US-11-039-767-4
US-11-031-485-123
US-11-031-485-123
US-11-031-485-123
US-11-031-485-123
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US-11-031-485-131
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Chen, Prancine
APPLICANT: Chen, Rancine
APPLICANT: Gazit, Gadi
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Best Local Similarity 100.0
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: homo sapiens
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US-10-041-860-221
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1251.741 Million cell updates/sec
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| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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1 DIVWTQSPLSLPVTPGBPAS.....MQALQSLMCSFGQGTKLEIK
                                                                                                                                                                                                                                                                                                   April 25, 2007, 04:18:18 ; Search time 42 Seconds
                                       version 6.2.1 - 2007 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                            GenCore (c) 1993
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Maximum DB seq length: 200000000
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Match Length DB
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Score

Result Š ö

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Query Match
Best Local Similarity
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazir, Gadi
APPLICANT: Gazir, Gadi
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTIBODIES
TITLE OF 
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
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Best Local Similarity 100.
Matches 113; Conservative
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CRGANISM: homo sapiens
US-10-041-860-221
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US-10-041-860-255
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Best Local Similarity
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1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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Pred. No. 7.4e-45;
1; Mismatches 0; Indels 1
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APPLICANT: Gazit, Gadi
APPLICANT: Keyt, Bruce
APPLICANT: LaRochelle, William
APPLICANT: Lichentein, Henri
APPLICANT: Lichentein, Henri
APPLICANT: Lichentein, Henri
TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REPERENCE: ABGENIX. 052A
CURRENT FILING DATE: 2003-09-16
PRIOR PLLICATION NUMBER: 60/411,137
PRIOR PLLICATION NUMBER: 60/411,137
RIOR PLLICATION NUMBER: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 40
SEQ ID NO 40
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98.2%;
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Yang, Xiao-Dong
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Best Local Similarity 98.2<sup>3</sup>
Matches 112; Conservative
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CORGANISM: homo sapiens
US-10-041-860-322
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ORGANISM: homo sapiens
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RESULT 6 US-11-021-715-89

Sequence 40, Application US/10665383 Publication No. US20040141969A1 GENERAL INFORMATION: APPLICANT: Floege, Juergen

US-10-665-383-40

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61 SGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCMQALQII---TFGQGTRLEIK 111
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Publication No. US20040018198A1
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US-10-309-762-165
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CURRENT APPLICATION NUMBER: US/11/021,715

CURRENT APPLICATION NUMBER: US/11/233

PRIOR PLING DATE: 2003-07-03

PRIOR PLING DATE: 2002-07-03

PRIOR PLING DATE: 2002-07-03

PRIOR PLING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 153

SOFTWARE: PATENT VERSION 3.2

SEQ ID NOS: 153
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APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Ling Chen
APPLICANT: Meina Ling
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: Xiao Chi Jia
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CURRENT APPLICATION: AND USES THEREOF
FILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ABGENIX: 072A
CURRENT APPLICATION UNMBER: US/10/726,332
CURRENT FILING DATE: 2003-12-02
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 222
SOFTWARE FEASESQ for Windows Version 4.0
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Pred. No. 8.2e-43;
4; Mismatches 3,
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Publication No. US20050058649A1
GENERAL INFORMATION:
Sequence 89, Application US/11021715
Publication No. US20050208596A1
GENERAL INFORMATION:
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Best Local Similarity 93.8%;
Matches 106; Conservative
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US-10-726-332-215
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LENGTH: 112
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Sequence 88, Application US/11021715

Sequence 88, Application US/11021715

Publication No. US2005020856A1

GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

FILE SEPERANCE: 053893-5050

CURRENT APPLICATION NUMBER: US/11/021,715

CURRENT APPLICATION NUMBER: PCT/US03/21304

PRIOR FILING DATE: 2003-07-03

PRIOR FILING DATE: 2003-07-03

PRIOR APPLICATION NUMBER: 60/411,694

PRIOR FILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 153

SOFTWARE: Patentin Version 3.2

SEQ ID NOS: 153

SEQ ID NOS: 153
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APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Gulo, Michael
TITLE OF INVENTION: (A.I.)
FILE REFERENCE: ABGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (A.I.)
FILE REFERENCE: ABGRIN: 0.27A
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE FEARLSEQ FOR WINDOWS Version 4.0
SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.1%; Score 549; DB 6; Length 113; 92.9%; Pred. No. 2.4e-42;
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1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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92.9%;
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Matches 107; Conservative
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US-11-021-715-92
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Best Local Similarity
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US-11-021-715-92
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TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
FILE REPERENCE: 053093-5050
CURRENT PILING DATE: 2004-12-23
FRIOR RILING DATE: 2003-07-03
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-09-18
NIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PALENTIN Version 3.2
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                                61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT---PFGQGTKLEIK 110
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APPLICANT: GLADUE, RONALD P.
APPLICANT: CIADUE, RONALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT APPLICATION NUMBER: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
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                                                                                                                                                                                                 ; Sequence 74, Application US/11021715; Publication No. US20050208596A1; GENERAL INFORMATION:
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Best Local Similarity 94.7<sup>1</sup>
Matches 107; Conservative
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US-10-292-088-104
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US-11-021-715-74
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Best Local Similarity
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SEQ ID NO 104
LENGTH: 112
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US-11-021-715-74
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Sequence 92, Application US/11021715

Sequence 92, Application US/11021715

Publication No. US2005020856A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: EQ/394,352
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.2
SEQ ID NO 92
LENGTH: 112
TYPE: PRI
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Publication No. US20050208596A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: AUTOANTIBODIES AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
TITLE REFERENCE: 053893-5050
CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT FILING DATE: 2004-12-23
FRIOR APPLICATION NUMBER: 60/394,352
FRIOR APPLICATION NUMBER: 60/394,352
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.2
LENGTH: 112
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61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
                                                     61 SGVPDRFSGSGSGTDPTLKISRVEAEDVGVYYCMQALQT-PYTFGQGTKLEIK 112
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Pred. No. 3.2e-42;
3; Mismatches 2;
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT-PYTFGQGTKLEIK 112

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                                                         1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHTNGYNYLDWYVQKPGQSPQLLIYLGSNRA
                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQXPGQSPQLLIYLGSNRA
 Gaps
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                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGYYYCMQALQTL1-TFGGGTRLEIK 112
                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.8%; Score 547.5; DB 5; Length 113; Best Local Similarity 94.7%; Pred. No. 3.2e-42; Matches 107; Conservative 3; Mismatches 2; Indels 1
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/490,324
PILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
Mismatches
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NAME: James F. Haley, Jr., Esq.
REGISTRATION UNMER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/834,397
FILING DATE: 29-Apr-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDURSS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 113 amino acids
 7;
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SEQUENCE CHARACTERISTICS
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105; Conservative
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                                                                                                                                                                                                          RESULT 14
US-10-834-397-15
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1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
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                                                                                                                    APPLICANT: Ling Chen
APPLICANT: Ven-Wah R. Lee
APPLICANT: Weina Liang
APPLICANT: Neina Liang
APPLICANT: Xiao-Chi Jia
APPLICANT: Xiao-Chi Jia
APPLICANT: Xiao-Chi Jia
APPLICANT: Nacerini
APPLICANT: MANTHEDIES DIRECTED TO PHOSPHOLIPASE A2
TITLE OF INVENTION: AND USES THEREOF
FILE REPREBENCE: ABGENIX.072A
CURRENT APPLICATION NUMBER: US/10/726,332
CURRENT FILING DATE: 2003-12-02
PRIOR FILING DATE: AND USES THE ABERTOR FILING DATE: NUMBER: N/a
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
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Pred. No. 3.5e-42;
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Sequence 24, Application US/10726332
Publication No. US20050058649A1
GENERAL INFORMATION:
                                                                            APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.7%;
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Best Local Similarity 92.9
Matches 105; Conservative
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ORGANISM: Homo sapiens
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Thu Apr 26 11:39:45 2007
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Sequence 225, App
Sequence 322, App
Sequence 19, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 98, Appl
Sequence 106, Appl
Sequence 104, Appl
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Sequence 128, Appl
Sequence 128, Appl
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639, App
73, Appl
81, Appl
89, Appl
97, Appl
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                                                                                          April 25, 2007, 04:23:02 ; Search time 44 Seconds (without alignments) 533.620 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US01_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US01_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US01_NEW_PUB.pep:*
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd
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US-11-109-181-221

US-11-109-181-325

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US-11-428-895-19

US-11-428-895-25

US-11-396-178-98

US-11-396-178-98

US-11-31-917-104

US-11-21-917-104

US-11-256-332-128

US-11-256-332-128

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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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483, App
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US-11-311-939-215
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US-11-211-917-28
US-11-211-917-28
US-11-211-917-32
US-11-593-280-4
US-11-593-280-4
US-11-593-280-4
US-11-337-300-437
US-11-337-300-437
US-11-337-300-437
US-11-311-939-483
US-11-109-181-250
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                                                                    APPLICANT: Organian, Jose R.F.
APPLICANT: Corvaland, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao
APPLICANT: Peng, Xiao
APPLICANT: Reng, Xiao
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTHEODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTHEODIES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR FILING DATE: 2005-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 113
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Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0;
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; Sequence 221, Application US/11109181
; Publication No. US20060293506A1
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; Sequence 30, Application US/11109181; Publication No. US20060293506A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                           APPLICANT: Chen, Francine
APPLICANT: Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTHENEDE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ADDITION
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR APPLICATION NUMBER: US/10/041,860
MUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CONTAINED:
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Weber, Xiao-Dong
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
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CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR PELLING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 255, Application US/11109181 Publication No. US20060293506A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 113; Conservative
                        Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: homo sapiens
US-11-109-181-221
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Feng, Xiao
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LENGTH: 113
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Sequence 19, Application US/11428895

Publication No. US20070003554A1

GENERAL INFORMATION:

APPLICANT Miller, Jonathan L

TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions

TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha

FILE REFERENCE: 011.00231

CURRENT APPLICATION NUMBER: US/11/428,895

CURRENT FILING DATE: 2006-07-06

PRIOR APPLICATION NUMBER: US/09/430,048

PRIOR APPLICATION NUMBER: US 60/106,275

PRIOR APPLICATION NUMBER: US 60/106,275

PRIOR PRIOR PLING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 62

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19

LENGTH: 114
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                                                                                                                                                                                      APPLICANT: Yang, Atao-Dong
APPLICANT: Yang, Atao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Becabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: WINTER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR PRILING DATE: 2005-04-18
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 322
LENGTH: 114
Sequence 322, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
                                                                                                APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 98.2
Matches 112, Conservative
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1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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Publication No. US20060275211A1
GREERAL INFORMATION:
APPLICANT: JAKOBOVITS, Aya
APPLICANT: KANNER, Steven B.
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: PEREZ-VILLAR, Juan
                                                                                                                                                                                                       Sequence 98, Application US/11396178
Publication No. US20060275211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       APPLICANT: JAKOBOVITS, Aya
APPLICANT: KANNER, Steven B.
APPLICANT: CHALLITA-EID, Pia M.
APPLICANT: PEREZ-VILLAR, Juan
                                                                                                                                                                                                                                                                                                                                                                        SATPAEV, Daulet
RAITANO, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.2
Best Local Similarity 93.8
Matches 106; Conservative
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GUDAS, Jean
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-11-433-924-268

i Sequence 268. Application US/11433924

j Publication No. US20060266112A1

j GENERAL INFORMATION:
   APPLICANT: Foord, Orit

j APPLICANT: Foord, Orit

j APPLICANT: Foord, Orit

j APPLICANT: Foord, Orit

j APPLICANT: Foord Unit

j APPLICANT: Foord Unit

j APPLICANT: Poord, Orit

j TITLE OF INVENTION: USY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION OFHER DISORDERS

j TITLE OF INVENTION: OFHER DISORDERS

j TITLE OF INVENTION: OFHER DISORDERS

j TITLE OF INVENTION: OFHER DATE: 2006-05-12

j FILE APPLICATION NUMBER: US/11/433,924

cURRENT APPLICATION NUMBER: US/06-05-16

j PRIOR APPLICATION NUMBER: US 60/681,846

j PRIOR FILING DATE: 2005-05-16

k NUMBER OF SEQ ID NOS: 419

con the No. 100
                                                                                                                                                                                                                                               APPLICANT: Miller, Jonathan L
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha
FILE REFERENCE: 011.00231
CURRENT APPLICATION NUMBER: US/11/428,895
CURRENT APPLICATION NUMBER: US/09/430,048
PRIOR APPLICATION NUMBER: US/09/430,048
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: RELEASE PATENTION VET. 2.1
SOFTWARE: Patentin Vet. 2.1
LENGTH: 131
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                     61 SGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKLEIK 113
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Pred. No. 1.4e-44;
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                                                                                                                                                                               ; Sequence 25, Application US/11428895; Publication No. US20070003554A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 93.8
Matches 106; Conservative
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Matches 106; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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LENGTH: 111
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8 DIVMTÓSPLSLPVTPGEPASISCRSSÓSLLHSNGYNYLDWYLÓKÞGOSPÓLLIYLGSNRA
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTI--TFGQGTRLEIK 111
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TITLE OF INVENTION: BIND TO 161P2F10B PROTEINS
FILE REPERENCE: 511582006221
CURRENT APPLICATION NUMBER: US/11/396,178
CURRENT FILING DATE: 2006-03-31
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FLING DATE: 2001-11-07
PRIOR FLING DATE: 2001-11-07
PRIOR FLING DATE: 2001-11-07
PRIOR FLING DATE: 2001-13-17
PRIOR FILING DATE: 2005-03-31
PRIOR FILING DATE: 2005-03-31
PRIOR FILING DATE: 2005-03-31
PRIOR FILING DATE: 2005-07-00
NUMBER OF SEQ ID NOS: 177
SOFFWARE: FREESEQ FOR Windows Version 4.0
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93.8%; Pred. No. 5.8e-44;
tive 5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 211
; OTHER INFORMATION: Xaa = Any amino acid.
US-11-396-178-98
                                                                                                                                                                                                                                                                                                                                                                                                                       MORRISON, Robert Kendall
MORRISON, Karen Jane Meyrick
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RAITANO, Arthur B.
MORRISON, Robert Kendall
MORRISON, Karen Jane Meyrick
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT--PTFGQGTKLEIK 111
                                                                            RESULT 11
US-11-211-917-104
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Publication No. US20070003554A1

Sequence 20, Application US/1003554A1

Sequence 20, Application No. US20070003554A1

Septimization No. US20070003554A1

SERREAL INTORNATION:

TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha

TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha

FILE REFERENCE: 011.00231

CURRENT APPLICATION NUMBER: US/11/428,895

CURRENT APPLICATION NUMBER: US/09/430,048

PRIOR APPLICATION NUMBER: US 60/106,275

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 62

SOUTWARE PATENT NOS: 62

SOUTWARE PATENT NOS: 62
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          APPLICANI: JLP, ALLO
APPLICANI: JLP, ALLO
APPLICANI: GUDAS, Jean
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
TITLE OF INVENTION: BIND TO 161P2F10B PROTEINS
FILE REPERENCE: 51158206221
CURRENT APPLICATION NUMBER: US/11/396,178
FRICK APPLICATION NUMBER: 10/291,241
PRIOR APPLICATION NUMBER: 10/291,241
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2005-03-31
PRIOR PILING DATE: 2005-03-31
PRIOR PILING DATE: 2005-07-20
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FaetSEQ for Windows Version 4.0
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Pred. No. 4.4e-44;
3; Mismatches 1; Indels
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US-11-396-178-156
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Best Local Similarity 94.77
Matches 107; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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NAME/KEY: VARIANT
LOCATION: 211
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US-11-428-895-20
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1 DIVWIQSPLSLPVIPGEPASISCRSSQSLIHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
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APPLICANT: Strohl, William R.
APPLICANT: Wang, Fubao
TITLE OF INVENTION: ANTI-ADDL ANTIBODIES AND USES THEREOF
FILE REFERENCE: MRK0002US
CURRENT APPLICATION NUMBER: US/11/256,332
CURRENT FILING DATE: 2005-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.8%; Score 547.5; DB 7; Best Local Similarity 94.7%; Pred. No. 4.8e-44; Matches 107; Conservative 3; Mismatches 2;
CURRENT FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: US 60/621,776
PRIOR PILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US 60/652,538
PRIOR FILING DATE: 2005-02-14
PRIOR PLING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: US 60/695,528
PRIOR PLING DATE: 2005-06-30
PRIOR PLING DATE: 2005-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 128, Application US/11256332 Publication No. US20060228349A1 GENERAL INFORMATION:
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Chen Dodson, Elizabeth
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Klein , William R.
Krafft , Grant A.
Liambert , Mary P.
Liamb, Xiaoping
Pray, Todd R.
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APPLICANT: An, Zhiqiang
APPLICANT: Bett, Andrew J.
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ORGANISM: Homo sapiens
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Strohl, William
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Best Local Similarity 93.8
Matches 106; Conservative
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Matches 106; Conservative
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US-11-311-939-639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/11369641
Publication No. US20060258852A1
GENERAL INFORMATION No. US20060258852A1
GENERAL INFORMATION No. US20060258852A1
TITLE OF INVENTION: METHODS OF HUMANIZING IMMUNOGLOBULIN VARIABLE REGIONS
TITLE OF INVENTION: DEFERMINING REGIONS
TITLE OF INVENTION: DEFERMINING REGIONS
TITLE OF INVENTION: DEFERMINING REGIONS
CURRENT APPLICATION NUMBER: US/11/369,641
CURRENT FILING DATE: 2006-03-06
PRIOR FILING DATE: 2006-03-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
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                                                                                                                                                                DB 7; Length 112;
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                                                                                                                                                                          4; Mismatches
                                                                                                                                                                Score 546.5;
Pred. No. 6e-
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Chen Dodson, Elizabeth
Kinney, Gene
Klein, William R.
Krafft, Grant A.
Lambert, Mary P.
Liang, Xiaoping
Pray, Todd R.
Shughrue, Paul
NUMBER OF SEQ ID NOS: 322
SOFTWARE: Patentin version 3.3
SEQ ID NO 128
LENGTH: 112
                                                                                                                                                              Query Match

Best Local Similarity 93.8%;
Matches 106; Conservative
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Best Local Similarity 93.84
Matches 106; Conservative
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APPLICANT: An, Zhiqiang
APPLICANT: Bett, Andrew J.
                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-256-332-128
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; ORGANISM: Homo sapiens
US-11-369-641-4
                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Publication No. US20060246071A1
GENERAL INFORMATION:
APPLICANT: Green, Larry L.
APPLICANT: Zhou, Qing
APPLICANT: Keyt, Bruce A.
APPLICANT: Bmery, Stephen
APPLICANT: Blakey, David C.
TITLE OF INVENTION: ANTIBODIES DIRECTED TO ANGIOPOIETIN-2
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ABXAZ.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
APPLICANT: Wang, Fubao
TITLE OF INVENTION: ANTI-ADDL ANTIBODIES AND USES THEREOF
FILE REFERENCE: MRK0002US
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                                                                     FILE KEFERENCE: MAKOUGUSUS
CURRENT PAPLICATION NUMBER: US/11/256,332
CURRENT FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: US 60/621,776
PRIOR PILING DATE: 2004-10-25
PRIOR PILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-02-14
PRIOR FILING DATE: 2005-06-30
PRIOR PILING DATE: 2005-06-30
PRIOR PILING DATE: 2005-06-30
PRIOR PILING DATE: 2005-06-30
NUMBER OF SEQ ID NOS: 322
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 118
LENGTH: 113
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CURRENT FILING DATE: 2005-12-19
PRIOR APPLICATION NUMBER: US 60/638,354
PRIOR FILING DATE: 2004-12-21
PRIOR FILING DATE: 2005-08-25
NUMBER OF SEQ ID NOS: 662
SEQ ID NO 639
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPI-TFGQGTRLEIK 112

Search completed: April 25, 2007, 04:27:43 Job time : 43.572 secs